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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:24:34 ; Search time 114.5 Seconds
(without alignments)
23.936 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186

Sequence: 1 MLKLGIDISNAIDLSNKASLAFLOKHLGLHKDFDQ 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_ll01.*
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21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	100.0	441	21	Human low density
2	186	100.0	442	16	Human T-cell lymph
3	182	97.8	440	22	Mouse-Human plasma
4	182	97.8	440	22	Mouse-Human plasma
5	182	97.8	441	16	Human acetyl hydro
6	182	97.8	441	16	Human acetyl hydro
7	182	97.8	441	16	Human acetyl hydro
8	182	97.8	441	16	Human acetyl hydro
9	182	97.8	441	16	Human acetyl hydro
10	182	97.8	441	16	Human acetyl hydro
11	182	97.8	441	16	Human acetyl hydro

12	182	97.8	441	16	Human acetyl hydro
13	182	97.8	441	16	Human acetyl hydro
14	182	97.8	441	16	Human acetyl hydro
15	182	97.8	441	16	Human plasma plate
16	182	97.8	441	18	Human platelet-act
17	182	97.8	441	18	Human plasma plate
18	182	97.8	441	18	Human platelet-act
19	182	97.8	441	19	Human plasma plate
20	182	97.8	441	20	Human plasma plate
21	182	97.8	441	20	Human PAF-AH prote
22	182	97.8	441	21	Human platelet-act
23	182	97.8	441	21	Human platelet-act
24	182	97.8	441	21	Human PAF-AH prote
25	182	97.8	441	22	Human plasma plate
26	182	97.8	441	22	Human plasma plate
27	182	97.8	441	22	Human plasma plate
28	182	97.8	441	22	Human plasma plate
29	182	97.8	441	22	Human plasma plate
30	182	97.8	441	22	Human plasma plate
31	182	97.8	441	22	Human plasma plate
32	182	97.8	441	22	Human plasma plate
33	182	97.8	441	22	Human plasma plate
34	182	97.8	441	22	Human plasma plate
35	182	97.8	441	22	Human plasma plate
36	182	97.8	441	22	Human plasma plate
37	182	97.8	441	22	Human plasma plate
38	182	97.8	441	22	Human plasma plate
39	182	97.8	441	22	Human plasma plate
40	163	87.6	171	16	Platelet-activatin
41	163	87.6	171	16	Murine (rat) plate
42	163	87.6	171	18	Rat platelet-activ
43	163	87.6	171	18	Rat partial plasma
44	163	87.6	171	19	Rat plasma platele
45	163	87.6	171	20	Rat PAF-AH C-termi
					Rodent PAF-AH prot

ALIGNMENTS

RESULT 1
ID AAB01942 standard; Protein; 441 AA.
XX AAB01942;
AC AAB01942;
DT 18-SEP-2000 (first entry)

XX Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).
DE Human; low density lipoprotein associated phospholipase A2;
KW LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;
KW short chain phospholipid; serine-dependant phospholipase;
KW inflammation; proinflammatory; anti inflammatory; drug screening;
KW antibody; diagnosis.

XX Homo sapiens.
OS WO2000024910-A1.
PN 04-MAY-2000.
PD 27-OCT-1999; 99WO-GB03551.
PF 28-OCT-1998; 98GB-0023647.
PR 28-OCT-1998; 98GB-0023648.
XX (SMIK) SMITHKLINE BEECHAM PLC.
PI Boyd H, Tew DG;
XX WPI: 2000-350749/30.
DR N-PSDB; AAA52357.
XX

PT Recombinant low density lipoprotein associated phospholipase A2, used
 PT to produce antibodies for diagnostics, is purified using a Blue
 XX Sepharose and Q Sepharose column.
 PS Claim 6b; Page 17; 28pp; English.
 XX
 CC The present sequence represents human LDL-PLA2. The invention
 CC relates to a method for purifying recombinant low density lipoprotein-
 CC associated phospholipase A2 (LDL-PLA2). The method comprises
 CC applying a cell extract, supernatant or solution containing the
 CC recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the
 CC eluate to a Blue Sepharose column, and applying that eluate to a Q
 CC Sepharose column. The invention also provides a process which
 CC additionally comprises the prior steps of constructing a vector
 CC comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment
 CC thereof, expressing the tagged protein in a host cell, isolating the
 CC tagged protein from the harvest medium or cell lysate, purifying the
 CC protein using a metal matrix affinity column (preferably a nickel
 CC column), and removing the histidine tag by protease cleavage. LDL-PLA2,
 CC also known as plasma PAF acetyl hydroxylase, is a serine-dependent
 CC phospholipase which catalyses the hydrolysis of phospholipids with short
 CC chain acyl groups at the sn-2 position. Its in vivo role is not known -
 CC due to its ability to hydrolyse both phospholipids with short chain sn-2
 CC substituents (which often arise from oxidative cleavage of longer chain
 CC sn-2 substituents) and PAF, it may be either a pro-inflammatory enzyme or
 CC an anti-inflammatory enzyme, depending on the precise in vivo role
 CC adopted. LDL-PLA2 can be used in structural and mechanistic studies to
 CC elucidate the activity of the enzyme in vivo. The enzyme may be used to
 CC screen and identify compounds which modulate its activity, and to raise
 CC antibodies for use in diagnostics.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 186; DB 21; Length 441;
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHGLHKHDFDQ 37
 DB 368 mlklkgdidsnaaidlsnkaslaflqkhlghkhdq 404

RESULT 2
 AAR64928
 ID AAR64928 standard; Protein; 442 AA.
 XX
 AC AAR64928;
 XX
 DT 18-AUG-1995 (first entry)
 XX
 DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
 XX
 KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;
 KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 ER Key Location/Qualifiers
 FT Peptide 25..31
 FT /note= "Peptide 4"
 FT Peptide 115..133
 FT /note= "Peptide 3"
 FT Peptide 298..327
 FT /note= "Peptide 2"
 FT Peptide 368..393
 FT /note= "Peptide 1"
 XX
 PN WO9500649-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 24-JUN-1994; 94WO-GB01374.

XX 25-JUN-1993; 93GB-0013144.
 PR 11-JAN-1994; 94GB-0000413.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Gloger IS, Hickey DMB, Lawrence GMP, Macphee CH;
 PI Rice SQJ, Southan CD, Tew DG;
 XX
 DR WPI; 1995-052086/07.
 DR N-PSDB; AA081780.
 XX
 PT Purified lipoprotein associated phospholipase A2 - used to
 PT develop prods. for diagnosis and therapy, partic. inhibitors for
 PT treatment of atherosclerosis
 XX
 PS Claim 8; Page 19; 29pp; English.
 XX
 CC This sequence encodes an enzyme which may be used in a method of
 CC screening compounds to identify those compounds which inhibit
 CC Lp-PLA2 which involves contacting isolated Lp-PLA2 with a test
 CC compound and measuring the rate of turnover of an enzyme substrate
 CC as compared with the rate of turnover in the absence of the test
 CC compound.
 XX
 SQ Sequence 442 AA;
 Query Match 100.0%; Score 186; DB 16; Length 442;
 Best Local Similarity 100.0%; Pred. No. 3.8e-19;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHGLHKHDFDQ 37
 DB 368 mlklkgdidsnaaidlsnkaslaflqkhlghkhdq 404

RESULT 3
 AAE00782
 ID AAE00782 standard; Protein; 440 AA.
 XX
 AC AAE00782;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHCl.
 XX
 KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 ER Key Location/Qualifiers
 FT Region 1..97
 FT /note= "Corresponds to N-terminal 97 amino acids of mouse
 FT plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 FT 98..440
 FT /note= "Corresponds to C-terminal 343 amino acids of
 FT human plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 XX
 PN US6203790-B1.
 XX
 PD 20-MAR-2001.
 XX
 PF 23-MAY-2000; 2000US-0577758.
 XX
 PR 07-JUN-1995; 95US-0480658.
 PR 22-JAN-1998; 98US-0010715.
 PR 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
XX Wilder CL;
XX WPI; 2001-280610/29.
XX N-PSDB; AAD04168.
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
XX administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
XX supplement endogenous PAF-AH activity and to inactivate pathological
XX amounts of PAF
XX
XX Example 8; Column -: 54pp; English.
XX
XX The present sequence is mouse-human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid
XX pRC/PH.MHC1.
XX The invention relates to human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
XX invention also relates to method of treating a mammal susceptible to
XX or suffering from septicemia. PAF functions in normal physiological
XX processes such as inflammation, haemostasis and parturition. PAF-AH
XX specific antibodies are used in the diagnostic methods to detect abnormal
XX levels of PAF-AH in serum and also for treating the pathological
XX inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
XX shock and arthritis. PAF-AH antibody is also useful for screening a
XX genetic lesion in the human plasma PAF-AH gene, which occurs due to the
XX replacement of nucleotide G to T at position 996 within exon 9 resulting
XX in replacement of amino acid Val to Phe at position 279. Thus the
XX deficiency of PAF-AH activity is due to the genetic lesion in human
XX plasma PAF-AH gene.
XX
XX Sequence 440 AA;
SQ

Query Match 97.8%; Score 182; DB 22; Length 440;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLKLGKIDSNAAIDLSNKSALFLQKHGLHKDFDQ 37
Db 367 mlkkgidsnvaidslnksalflqkghlkhkdfdg 403

RESULT 4
AAE00783
ID AAE00783 standard; Protein; 440 AA.
XX
XX AAE00783;
XX
XX 02-JUL-2001 (first entry)
XX
XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.
XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
XX anti-inflammatory; septicemia; inflammation; haemostasis; parturition;
XX asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
XX
XX Chimeric - Mus sp.
XX Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..40
XX /note= "Corresponds to N-terminal 40 amino acids of mouse
XX plasma platelet-activating factor acetylhydrolase
XX (PAF-AH)"
XX Region 41..440
XX /note= "Corresponds to C-terminal 400 amino acids of
XX human plasma platelet-activating factor acetylhydrolase
XX (PAF-AH)"
XX

XX US6203790-B1.
XX 20-MAR-2001.
XX 23-MAY-2000; 2000US-0577758.
XX 07-JUN-1995; 95US-0480658.
XX 22-JAN-1998; 98US-0010715.
XX 06-OCT-1993; 93US-0133803.
XX 06-OCT-1994; 94US-0318905.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
XX Wilder CL;
XX WPI; 2001-280610/29.
XX N-PSDB; AAD04169.
XX Treating a mammal susceptible to or suffering from septicemia comprises
XX administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
XX supplement endogenous PAF-AH activity and to inactivate pathological
XX amounts of PAF
XX
XX Example 8; Column -: 54pp; English.
XX
XX The present sequence is mouse-human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid
XX pRC/PH.MHC2.
XX The invention relates to human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
XX invention also relates to method of treating a mammal susceptible to
XX or suffering from septicemia. PAF functions in normal physiological
XX processes such as inflammation, haemostasis and parturition. PAF-AH
XX specific antibodies are used in the diagnostic methods to detect abnormal
XX levels of PAF-AH in serum and also for treating the pathological
XX inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
XX shock and arthritis. PAF-AH antibody is also useful for screening a
XX genetic lesion in the human plasma PAF-AH gene, which occurs due to the
XX replacement of nucleotide G to T at position 996 within exon 9 resulting
XX in replacement of amino acid Val to Phe at position 279. Thus the
XX deficiency of PAF-AH activity is due to the genetic lesion in human
XX plasma PAF-AH gene.
XX
XX Sequence 440 AA;
SQ

Query Match 97.8%; Score 182; DB 22; Length 440;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLKLGKIDSNAAIDLSNKSALFLQKHGLHKDFDQ 37
Db 367 mlkkgidsnvaidslnksalflqkghlkhkdfdg 403

RESULT 5
AAR73048
ID AAR73048 standard; Protein; 441 AA.
XX
XX AAR73048;
XX
XX 06-DEC-1995 (first entry)
XX Human acetyl hydrolase (AH) mutant C291S.
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX

FT Misc-difference 291
/note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGIDISNAADISNKSASLAFLOKHLGLHKDFDQ 37

Db 368 mlkkgidsnvaidslnksaslaflqhlghkdfdq 404

RESULT 6

AAR73049
ID AAR73049 standard; Protein; 441 AA.

XX AAR73049;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C334S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 334
/note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGIDISNAADISNKSASLAFLOKHLGLHKDFDQ 37

Db 368 mlkkgidsnvaidslnksaslaflqhlghkdfdq 404

RESULT 7

AAR73050
ID AAR73050 standard; Protein; 441 AA.

XX AAR73050;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C407S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 407
/note= "Wild-type Cys is substd. by Ser."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating

PT inflammatory diseases, e.g. pleurisy
 XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNNAIDLSNKKASLAFLOKHLGHLKDFDQ 37
 |||||
 DB 368 mlklkgdidsnvaidslnkksafqlqhlghkdfdq 404

RESULT 8

AAR71920
 ID AAR71920 standard; Protein; 441 AA.

AC AAR71920;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant S108A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108
 FT /note= "Wild-type Ser is substnd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNNAIDLSNKKASLAFLOKHLGHLKDFDQ 37
 |||||
 DB 368 mlklkgdidsnvaidslnkksafqlqhlghkdfdq 404

RESULT 9

AAR71921
 ID AAR71921 standard; Protein; 441 AA.

XX AAR71921;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S273A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 273
 FT /note= "Wild-type Ser is substnd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
 Best Local Similarity 97.3%; Pred. No. 1.5e-18;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQ 37
|||||
Db 368 mklkgdidsnvaidslnksaslaflqkhlghkdfdq 404

RESULT 10

AAR71922
ID AAR71922 standard; Protein; 441 AA.

XX AAR71922;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant D296A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 296
FT /note= "Wild-type Asp is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match

Best Local Similarity 97.8%; Score 182; DB 16; Length 441;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQ 37
|||||

Db 368 mklkgdidsnvaidslnksaslaflqkhlghkdfdq 404

RESULT 11

AAR71923
ID AAR71923 standard; Protein; 441 AA.

XX AC

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant D338A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 338
FT /note= "Wild-type Asp is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match

Best Local Similarity 97.8%; Score 182; DB 16; Length 441;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQ 37
|||||

Db 368 mklkgdidsnvaidslnksaslaflqkhlghkdfdq 404

RESULT 12

AAR71924

ID AAR71924 standard; Protein; 441 AA.

XX AAR71924;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant H351A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

```
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 351
XX FT /note= "Wild-type His is substd. by Ala."
XX
XX PN W09509921-A.
XX PD 13-APR-1995.
XX
XX PF 06-OCT-1994; 94WO-US11340.
XX PR 06-OCT-1993; 93US-0133803.
XX PA (ICOS-) ICOS CORP.
XX
XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX PF New nucleic acid encoding platelet activating factor,
XX PT acetyl:hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX
XX PS Example 10; ; 88pp; English.
XX
XX CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX
XX SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASLAFQKHLGHLKDFDQ 37
Db ||||||| ||||||| ||||||| ||||||| |||||||
368 mlklkgdidsnvaidslnkaskafqlqhlghkdfdq 404

RESULT 13
AAR73046
ID AAR73046 standard; Protein: 441 AA.
XX
XX AC AAR73046;
XX
XX DT 06-DEC-1995 (first entry)
XX
XX DE Human acetyl hydrolase (AH) mutant C67S.
XX
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 67
XX FT /note= "Wild-type Cys is substd. by Ser."
XX
XX PN W09509921-A.
XX PD 13-APR-1995.
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PF 06-OCT-1994; 94WO-US11340.
XX
XX PR 06-OCT-1993; 93US-0133803.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX PF New nucleic acid encoding platelet activating factor,
XX PT acetyl:hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX
XX PS Example 10; ; 88pp; English.
XX
XX CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX
XX SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNAAIDLSNKASLAFQKHLGHLKDFDQ 37
Db ||||||| ||||||| ||||||| ||||||| |||||||
368 mlklkgdidsnvaidslnkaskafqlqhlghkdfdq 404

RESULT 14
AAR73047
ID AAR73047 standard; Protein: 441 AA.
XX
XX AC AAR73047;
XX
XX DT 06-DEC-1995 (first entry)
XX
XX DE Human acetyl hydrolase (AH) mutant C229S.
XX
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 229
XX FT /note= "Wild-type Cys is substd. by Ser."
XX
XX PN W09509921-A.
XX PD 13-APR-1995.
XX
XX PF 06-OCT-1994; 94WO-US11340.
XX
XX PR 06-OCT-1993; 93US-0133803.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX
XX WPI; 1995-155262/20.
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XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
XX
XX Example 10; : 88pp; English.
XX
CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.
XX
SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKAFLQKHLGHLKDFDQ 37
|||||
Db 368 mlkkgdidsnvaidlsnksaslaflqkhlghlkdfdq 404

RESULT 15
AAR71913
ID AAR71913 standard; Protein; 441 AA.
XX
XX AC AAR71913;
XX
XX DT 05-DEC-1995 (first entry)
XX
XX DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
XX
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN WO9509921-A.
XX
XX PD 13-APR-1995.
XX
XX PF 06-OCT-1994; 94WO-US11340.
XX
XX PR 06-OCT-1993; 93US-0133803.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX DR N-PSDB; AAQ87947.
XX
XX PT New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
XX
XX PS Claim 5; Page 53-54; 88pp; English.
XX
XX CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
XX CC is useful in the treatment of inflammatory diseases, in particular
XX CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
XX CC raising monoclonal antibodies specific for PAF-AH that are useful in
XX CC the diagnosis of such diseases.

XX
SQ Sequence 441 AA;

Query Match 97.8%; Score 182; DB 16; Length 441;
Best Local Similarity 97.3%; Pred. No. 1.5e-18;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKAFLQKHLGHLKDFDQ 37
|||||
Db 368 mlkkgdidsnvaidlsnksaslaflqkhlghlkdfdq 404

Search completed: March 9, 2002, 00:31:56
Job time: 442 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:26:19 ; Search time 47.03 seconds
(without alignments)
17.704 Million cell updates/sec

Title: US-09-922-067-1
Perfect score: 186
Sequence: 1 MLKUKGIDISNAIDLSNKASLAFLQKHLGHLKDFDQ 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_5/ptodata/2/iaa/5A-COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	186	100.0	37	2	US-08-557-892-1
2	186	100.0	37	2	US-08-387-858A-1
3	186	100.0	37	4	US-09-294-384B-1
4	182	97.8	441	1	US-08-470-187-8
5	182	97.8	441	1	US-08-318-905-8
6	182	97.8	441	1	US-08-483-232-8
7	182	97.8	441	1	US-08-483-140-8
8	182	97.8	441	2	US-08-485-938A-8
9	182	97.8	441	2	US-08-910-041-8
10	182	97.8	441	3	US-09-328-474-8
11	182	97.8	441	3	US-09-100-546-8
12	182	97.8	441	4	US-09-010-715-8
13	182	97.8	441	4	US-09-577-758-8
14	163	87.6	171	1	US-08-483-140-29
15	163	87.6	171	2	US-08-485-938A-31
16	155	83.3	444	1	US-08-483-140-28
17	155	83.3	444	2	US-08-485-938A-32
18	155	83.3	444	2	US-08-485-938A-33
19	148	79.6	440	1	US-08-483-140-27
20	148	79.6	440	2	US-08-485-938A-31
21	128	68.8	422	2	US-08-485-938A-34
22	73	39.2	392	2	US-08-886-152-1
23	71	38.2	392	2	US-08-886-152-3
24	52	28.0	419	1	US-08-330-154-2
25	51	27.4	2332	4	US-09-091-219-25
26	51	27.4	2247	4	US-09-091-219-2
27	51	27.4	15281	2	US-08-471-119A-2

28	50.5	27.2	2285	4	US-09-308-375-2	Sequence 2, Appli
29	49	26.3	972	3	US-08-335-844A-24	Sequence 24, Appli
30	48.5	26.1	2154	2	US-08-841-343-4	Sequence 4, Appli
31	47	25.3	509	3	US-08-369-822C-26	Sequence 26, Appli
32	47	25.3	509	3	US-08-582-776C-41	Sequence 41, Appli
33	47	25.3	509	3	US-08-434-831B-38	Sequence 38, Appli
34	46	24.7	92	1	US-08-347-492B-7	Sequence 7, Appli
35	46	24.7	92	2	US-08-798-143-7	Sequence 7, Appli
36	46	24.7	862	3	US-09-315-861-2	Sequence 2, Appli
37	46	24.7	1098	4	US-08-946-994-17	Sequence 17, Appli
38	46	24.7	1561	3	US-08-894-017-23	Sequence 23, Appli
39	45.5	24.5	1494	3	US-08-755-587-186	Sequence 186, App
40	45	24.2	334	6	5290690-11	Patent No. 5290690
41	45	23.9	881	4	US-09-413-814-44	Sequence 44, Appli
42	44.5	23.9	389	3	US-08-972-902-4	Sequence 4, Appli
43	44.5	23.9	428	2	US-08-889-711-4	Sequence 4, Appli
44	44.5	23.9	428	3	US-09-185-825-4	Sequence 2, Appli
45	44.5	23.9	763	2	US-08-889-711-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-557-892-1
; Sequence 1, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Glover, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE:

0; Gaps

0: Gaps

0: Caps

Query Match 97.8%; Score 182; DB 1; Length 441;
Best Local Similarity 97.3%; pred. NO. 2.le-19;
Matches 36; Conservative 0; Mismatches 1; Indels

Oy 1 MLKLGDDIDSNAAIDLSENKASLAFLOKHGLHLKDFDQ 37
 | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 368 MLKLGDDIDSNVAIDLSENKASLAFLOKHGLHLKDFDQ 404

RESULT 6
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431

```

; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: platelet-activating factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30

```

```

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-232-8

Query Match          97.8%; Score 182; DB 1; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.le-19;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQ 37
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Db 368 MLKLGKGDIDSNVAIDLSNKASLAFLOKHLGKDFDQ 404

RESULT 7
US-08-140-8
; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-8

Query Match          97.8%; Score 182; DB 1; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.le-19;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQ 37
   |||||
Db 368 MLKLGKGDIDSNVAIDLSNKASLAFLOKHLGKDFDQ 404

RESULT 8
US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match          97.8%; Score 182; DB 2; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.le-19;
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Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKLAFLOKHLGLHKDFDQ 37
 Db 368 MLKLGKGDIDSNVAIDLSNKLAFLOKHLGLHKDFDQ 404

RESULT 9

US-08-910-041-8
 ; Sequence 8, Application US/08910041
 ; Patent No. 5977308
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,041
 ; FILING DATE:

CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,232
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-910-041-8

Query Match 97.8%; Score 182; DB 2; Length 441;
 Best Local Similarity 97.3%; Pred. No. 2.1e-19;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKLAFLOKHLGLHKDFDQ 37
 Db 368 MLKLGKGDIDSNVAIDLSNKLAFLOKHLGLHKDFDQ 404

RESULT 10

US-09-328-474-8
 ; Sequence 8, Application US/09328474
 ; Patent No. 6045794
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S. D.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/328,474
 ; FILING DATE:

CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,232
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-328-474-8

Query Match 97.8%; Score 182; DB 3; Length 441;
 Best Local Similarity 97.3%; Pred. No. 2.1e-19;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKLAFLOKHLGLHKDFDQ 37
 Db 368 MLKLGKGDIDSNVAIDLSNKLAFLOKHLGLHKDFDQ 404

RESULT 11

US-09-100-546-8
 ; Sequence 8, Application US/09100546
 ; Patent No. 6099836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai

APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 609836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 97.8%; Score 182; DB 3; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.le-19;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNADLSNKSASLAFLOKHLGLHKDFDQ 37
DB 368 MLKLKGDIDSNADLSNKSASLAFLOKHLGLHKDFDQ 404

RESULT 12
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 97.8%; Score 182; DB 4; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.le-19;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLKGDIDSNADLSNKSASLAFLOKHLGLHKDFDQ 37
DB 368 MLKLKGDIDSNADLSNKSASLAFLOKHLGLHKDFDQ 404

RESULT 13
US-09-577-758-8
Sequence 8, Application US/09577758
Patent No. 6203790
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,758
FILING DATE:

Search completed: March 9, 2002, 00:32:58
Job time: 399 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:28:49 : Search time 53.53 Seconds
(without alignments)
52.652 Million cell updates/sec

Title: US-09-922-067-1
Perfect score: 186
Sequence: 1 MLKLGKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 37
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	182	97.8	441	2	S60247	platelet-activating
2	135	72.6	436	2	JC5021	platelet-activating
3	53	28.5	333	2	C85737	glycerolaldehyde-3-p
4	53	28.5	736	2	T01247	hypothetical prote
5	52.5	28.2	755	2	T34567	hypothetical prote
6	52	28.0	165	2	S14477	hypothetical prote
7	52	28.0	422	2	JC5325	glycerolaldehyde-3-p
8	51	27.4	306	1	S39151	methicillin resist
9	51	27.4	433	2	S05783	cyclin-suppressing
10	51	27.4	488	2	F84001	femA protein - Sta
11	51	27.4	660	2	T04416	glycine dehydrogen
12	51	27.4	698	2	A54796	sulfate transport
13	51	27.4	15281	2	S41309	regulatory protein
14	50.5	27.2	266	2	E64471	cyclosporin synth
15	50.5	27.2	395	2	A37118	hypothetical prote
16	50.5	27.2	758	2	S47866	methionine adenosy
17	50.5	27.2	2285	2	T12796	SPT21 protein - ye
18	50	26.9	115	2	A86853	probable transglyc
19	50	26.9	549	2	A39345	hypothetical prote
20	50	26.9	587	1	W2BEC9	alpha-mannosidase
21	49.5	26.6	441	2	A45565	gene 36 protein -
22	49	26.3	145	2	S62510	cysteine proteinas
23	49	26.3	175	2	B63250	hypothetical prote
24	49	26.3	260	2	E69956	hypothetical prote
25	49	26.3	285	2	T05777	phosphate ABC tran
26	49	26.3	333	1	DEHGGT	hypothetical prote
27	49	26.3	374	2	T44696	glycerolaldehyde-3-p
28	49	26.3	377	1	A44216	hypothetical prote
29	49	26.3	513	2	S65574	major envelope ant
						phosphate transpor

ALIGNMENTS

RESULT 1

S60247
platelet-activating factor acetylhydrolase precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999
C:Accession: S60247
R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Staforini, D.M.; Dietsch, G.; Schimpf, W.
Nature 374, 549-553, 1995
A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase
A:Reference number: S60247; MUID:95214779
A:Accession: S60247
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-441 <TJO>
A:Cross-references: EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g780133

Query Match 97.8%; Score 182; DB 2; Length 441;
Best Local Similarity 97.3%; Pred. No. 2.4e-17;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLKLGKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 37
|||||
Db 368 MLKLGKGDIDSNAAIDLSNKASLAFLQKHLGKDFDQ 404

RESULT 2

JC5021
platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig
N:Alternate names: PAF-acetylhydrolase
C:Species: Cavia porcellus (guinea pig)
C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C:Accession: JC5021; PC4207
R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Yokoyama, J. Biochem. 120, 838-844, 1996
A:Title: Cloning, expression and characterization of plasma platelet-activating factor
A:Reference number: JC5021; MUID:97103479
A:Accession: JC5021
A:Molecule type: DNA
A:Residues: 1-436 <KARI>
A:Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:g1644229
A:Accession: PC4207
A:Molecule type: protein
A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392
A:Experimental source: liver
C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite
C:Keywords: glycoprotein; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-436/product: platelet-activating factor-acetylhydrolase #status predicted <MAT>
F:76,200,324/Binding site: carboxylate (Asn) (covalent) #status predicted

A; Introns: 63/3; 107/1; 356/1

1 MLKLKGIDSNAADLSNKAFLQKH 28

DNA 5, 427-435, 1986

A;Accession: T04416
A;Status: preliminary; translated from GB/EMBL/DBJ

A.A.Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A.A.Note: only a part of the translation is shown
A.A.Note: the source is designated as *Tolypocladium inflatum*
C:Genetics:
A.Genetic code: SGC3
C:Superfamily: cyclosporin fungus cyclosporin synthetase; acetate--CoA ligase homology
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:532-1008/Domain: acetate--CoA ligase homology <ACLI1>
F:1029-1096/Domain: acyl carrier protein homology <ACP1>
F:1618-2069/Domain: acetate--CoA ligase homology <ACLI2>
F:2521-2594/Domain: acyl carrier protein homology <ACP2>
F:3115-3553/Domain: acetate--CoA ligase homology <ACLI3>
F:4014-4081/Domain: acyl carrier protein homology <ACP3>
F:4601-5057/Domain: acetate--CoA ligase homology <ACLI4>
F:5506-5573/Domain: acyl carrier protein homology <ACP4>
F:6094-6546/Domain: acetate--CoA ligase homology <ACLI5>
F:7003-7070/Domain: acyl carrier protein homology <ACP5>
F:7591-8042/Domain: acetate--CoA ligase homology <ACLI6>

F:78052-9157/Domain: acetate-CoA ligase homology <ACP1>
F:78558-9625/Domain: acyl carrier protein homology <ACP7>
F:10146-10586/Domain: acetate-CoA ligase homology <ACL8>
F:11055-11122/Domain: acyl carrier protein homology <ACP8>

F:11635-12106/Domain: acetate-CoA ligase homology <AC19>
F:12127-12194/Domain: acyl carrier protein homology <ACP9>
F:12715-13159/Domain: acetate-CoA ligase homology <AL10>
F:13623-13690/Domain: acyl carrier protein homology <AC10>

F;14698-14765/Domain: acyl carrier protein homology <ACII>
F:1060 2558 4045 5537 7034 8094 9589 11086 12158 13654 14729/Binding site: phospha-

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Query Match      27.4%   Score 51;   DB 2;   Length 15281;
Best Local Similarity 36.1%   pred. NO. 1.7e+03;
Matches 13; Conservative 6; Mismatches 13; Indels 4; Gaps 1;
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E64471

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: F64471

A. Authors: Kaine. B. P.: Borodovskiy. M.: Klenk. H. P.: Fraser. C. M.: Smith. H. O.: Wood.
C. Science 273, 1058-1073, 1996
D. Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
E. Sadow, P.W.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glode
F. Kirchner, R.; Overbeck, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glode
G. Reisch, C.I.; Overbeck, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glode

A: Accession: E64471
A: Status: preliminary
A: Status: nucleic acid sequence not shown
A: Status: translation not shown
A: Title: complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A: Reference number: A64300; MUID: 96337999

A;Residues: 1-266 <BUL>
 :Cross-references: CB:1167577. CB:177117. NID:02826400. PIDN:AAP002811. PID:015070

C:Genetics:
C:Cross-references: GB:06/377; GB:6/7117; NID:92626400; PID:AA659361.1; PID:91392
A:Map position: FOR1322159-1322959
A:Start codon: TTG
C:Superfamily: hypothetical protein MJ1374

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QY      3 KLGKDHDSNAAIDL---SNRASLAFIQKHGL 31
       :|||::||| ||| |
DB     193 RIKGHLCSNDAILDINSNMKKPELLIMHMGV 224
       :|||::||| ||| |
Query Match          27.2%; Score 50.5; DB 2; Length 266;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 6; Mismatches 11; Indels 3; Gaps 1;
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Query Match      27.2%  Score 50.5; DB 2; Length 395;
Best Local Similarity 41.0%; Pred. No. 31;
Matches 16; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

OY 1 MLKKGIDDSNAADISNKASLAFQKHGLG---HKDFD 35
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 64 MILLAGITSGRAIDYQKVREAF--KHIGYDSSKGF 100

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Search completed: March 9, 2002, 00:34:07
Job time: 318 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:19 ; Search time 30.16 Seconds
(without alignments)
44.980 Million cell updates/sec

Title: US-09-922-067-1

Perfect score: 186

Sequence: 1 MLKLGKIDISNAADLSNKSALFLQKHLGLHKDFDQ 37

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	97.8	441	1 PAF2_HUMAN	Q13093 h platelet-
2	155	83.3	444	1 PAF2_BOVIN	Q28017 b platelet-
3	155	83.3	444	1 PAF2_CANFA	Q28262 c platelet-
4	148	79.6	440	1 PAF2_MOUSE	Q60963 m platelet-
5	135	72.6	436	1 PAF2_CAVPO	P70683 g platelet-
6	128	68.8	422	1 PAF2_CHICK	Q90678 g platelet-
7	73	39.2	392	1 PAF2_BOVIN	P79106 bos taurus
8	71	38.2	392	1 PAF2_HUMAN	Q99487 homo sapien
9	53	28.5	333	1 G3P3_ECO57	P58072 escherichia
10	53	28.5	333	1 G3P3_ECOLI	P33898 escherichia
11	51	27.4	306	1 CSK1_SCHPO	P36615 schizosacch
12	51	27.4	433	1 FENA_STAUP	P14304 staphylococ
13	51	27.4	697	1 CRAC_DICDI	P35401 dictyosteli
14	50.5	27.2	395	1 METK_RAT	P18298 rattus norv
15	50.5	27.2	758	1 SP21_YEAST	P35209 saccharomyc
16	50	26.9	549	1 MNS1_YEAST	P32906 saccharomyc
17	50	26.9	587	1 UL25_HSVB	P28928 equine herp
18	49.5	26.6	441	1 CYSF_THEAN	P25781 theileria a
19	49.5	26.6	2156	1 ORP1_HUMAN	P56715 homo sapien
20	49	26.3	145	1 YAF4_SCHPO	Q09858 schizosacch
21	49	26.3	175	1 Y002_ARCFU	Q03233 archaeoglob
22	49	26.3	260	1 Y0GK_BACSU	P46342 bacillus su
23	49	26.3	332	1 G3P3_THEMA	P17721 thermotoga
24	49	26.3	377	1 VENV_FOWPV	P36316 fowlpox vir
25	49	26.3	971	1 AMPN_HAECCO	Q10737 haemochnus
26	49	26.3	1151	1 KPC1_YEAST	P24583 saccharomyc
27	48.5	26.1	395	1 METK_HUMAN	P31153 homo sapien
28	48.5	26.1	2363	1 SPOC_MOUSE	Q62261 mus musculu
29	48.5	26.1	2364	1 SPOC_HUMAN	Q01082 homo sapien
30	48.5	26.1	4644	1 DYHC_MOUSE	Q9JBU4 mus musculu
31	48	25.8	338	1 G3P_LACDE	O32755 lactobacilli
32	48	25.8	556	1 YMC3_YEAST	Q03718 saccharomyc
33	48	25.8	1609	1 PM21_CHLPN	Q926u5 chlamydia p

34 47.5 25.5 277 1 PAF2_MAIZE
35 47.5 25.5 386 1 ICEA_XENLA
36 47.5 25.5 416 1 YTM1_BACSU
37 47.5 25.5 1211 1 EX5B_HAEIN
38 47 25.3 264 1 GIDB_SYNY3
39 47 25.3 390 1 Y109_NPVAC
40 47 25.3 400 1 CSD_METTH
41 47 25.3 447 1 Y341_CHLMU
42 47 25.3 1244 1 SLAL_YEAST
43 47 25.3 1966 1 MYSB_CAEEL
44 47 25.3 2204 1 RRPL_NDVB
45 47 25.3 2216 1 YCF2_EPIVI

P42057 zea mays (m
P55865 xenopus lae
O34980 bacillus su
P45157 haemophilus
Q55787 synchocyst
P41662 autographa
O27442 methanobact
Q9PKX0 chlamydia m
P32790 saccharomyc
P02566 caenorhabdi
P11205 newcastle d
P30072 epifagus vi

ALIGNMENTS

RESULT 1
ID PAF2_HUMAN STANDARD; PRT; 441 AA.
AC Q13093; Q15692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN PLA2G7 OR PAFAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.
RC TISSUE=Myeloid;
RX MEDLINE=95214779; PubMed=7700381;
RA Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,
RA Schimpf B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,
RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;
RA "Anti-inflammatory properties of a platelet-activating factor
acetylhydrolase.";
RL Nature 374:549-553(1995).
RP [2]
RC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Lymphoma;
RA Tew D.G., Southan C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,
RA Moores K., Gloger I.S., Macphie C.H.;
RA "Purification, properties, sequencing, and cloning of a lipoprotein-
associated, serine-dependent phospholipase involved in the oxidative
modification of low-density lipoproteins.";
RL Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
Gray P.W.;
RA "Plasma platelet-activating factor acetylhydrolase is a secreted
phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
RN [4]
RP VARIANT PHE-279.
RX MEDLINE=96259525; PubMed=8675689;
RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,
RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,
RA McIntyre T.M., Gray P.W., Prescott S.M.;
RA "Platelet-activating factor acetylhydrolase deficiency. A missense
mutation near the active site of an anti-inflammatory
phospholipase.";
RL J. Clin. Invest. 97:2784-2791(1996).
RN [5]

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VARIANT PHE-279.
MEDLINE=98430412; PubMed=9759612;
RX Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
RA Yoshimizu N., Fukushi K., Satoh K.;
RT *A mutation in plasma platelet-activating factor acetylhydrolase
RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
RT for hypertension.;
RL Thromb. Haemost. 80:372-375(1998).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
CC RESPONSES.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
-----
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or send an email to license@isb-sib.ch).
-----
EMBL: U20157; AAC50126.1; -
DR EMBL; U24577; AAB04170.1; -
DR MIM; 601690; -
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR000734; Lipase.
DR PROSITE: PS00120; LIPASE_SER: 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 441
FT FT PLATELET-ACTIVATING FACTOR
FT FT ACETYLHYDROLASE.
FT ACT_SITE 273 273 CHARGE RELAY SYSTEM.
FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
FT ACT_SITE 351 351 CHARGE RELAY SYSTEM.
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .).
FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
FT FT PROTEIN).
FT FT /FTIG-VAR_004268.
FT FT
FT MUTAGEN 108 108 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT MUTAGEN 273 273 S->A: LOSS OF ACTIVITY.
FT MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.
FT MUTAGEN 286 286 D->N: DIMINISHED ACTIVITY.
FT MUTAGEN 296 296 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.
FT MUTAGEN 304 304 D->A: NO CHANGE IN ACTIVITY.
FT MUTAGEN 338 338 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.
FT CONFLICT 379 379 V -> A (IN REF. 2).
SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

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PAFA_BOVIN	STANDARD;	PRT;	444 AA.
ID	Q28017;		
AC	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	PLATELET-ACTIVATING FACTOR ACETYLDIOLASE PRECURSOR (EC 3.1.1.47)		
DE	(PAF ACETYLDIOLASE) (PAF 2-ACVLDIOLASE) (LDL-ASSOCIATED		
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGlycerophosphocholine		
DE	ESTERASE) (1-ALKYL-2-ACETYLGlycerophosphocholine ESTERASE).		
GN	PLA2G7.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Splicein;		
RX	MEDLINE=96029630; PubMed=7592717;		
RA	Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,		
RA	McIntyre L.M., Stafford D.M., Prescott S.M., Gray P.W.;		
RT	"Plasma platelet-activating factor acetylhydrolase is a secreted		
RT	phospholipase A2 with a catalytic triad.";		
RL	J. Biol. Chem. 270:25481-25487(1995).		
CC	-1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)		
CC	BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY		
CC	INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT		
CC	RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN		
CC	PHOSPHOLIPIDS.		
CC	-1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +		
CC	H(2O) = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.		
CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR.		
CC	-1- TISSUE SPECIFICITY: PLASMA.		
CC	-1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,		
CC	HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	at the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL: U34247; AAC48483.1; ..		
DR	InterPro; IPR000379; Est_lip_thioest_actsite.		
DR	InterPro; IPR000734; Lipase.		
DR	PROSITE; PS00120; LIPASE_SER; 1.		
KW	Hydrolase; Lipid degradation; Glycoprotein; Signal.		
FT	SIGNAL	1	21
FT	CHAIN	22	444
FT	ACT_SITE	274	274
FT	ACT_SITE	297	297
FT	ACT_SITE	352	352
FT	CARBOHYD	60	60
FT	CARBOHYD	200	200
FT	CARBOHYD	424	424
FT	CARBOHYD	434	434
FT	SEQUENCE	444 AA;	50133 MW; 97689917BE2F4C38 CRC64;

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Q60963;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLDHROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLDHROLASE) (PAF 2-ACYLDHROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
DE PLA2G7 OR PAFAH.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RC MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
RA Gray P.W.;
RA "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2O) = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U34277; AAC52274.1; -.
DR MGD; MGI:1351327; Pla2g7.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 440 PLATELET-ACTIVATING FACTOR
FT ACT_SITE 272 273 ACETYLDHROLASE.
FT ACT_SITE 295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SQUONCH 440 AA; 149361 MW; C82A6RAD42FAR2ER CRC64.
SO

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Query Match 79.6%; Score 148; DB 1; Length 440;
Best Local Similarity 80.6%; Pred. No. 8.4e-13;
Matches 29; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LKLKGDIDSNAAIDLSENKASLAFLOKHGLHKLDFDQ 37
| | | | | | | | : | | | | | | | |
Db 368 LTILKEGIDSRAVDITNKASMAFLQKHGLGLOKDEO 403

RESULT 5
PAFA_CAVPO
ID PAFA_CAVPO
STANDARD:
PRT: 436 AA.

DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).
GN PAF2H2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase.";
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
RP TISSUE=Prostate;
RX MEDLINE=98161812; PubMed=9494101;
RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphee C.H.,
RA Moores K., Glover I.S., Tew D.G.;
RT "Expression, purification and characterization of a human
RT serine-dependent phospholipase A2 with high specificity for oxidized
RT phospholipids and platelet activating factor.";
RL Biochem. J. 330:1309-1315(1998).
RN [3]
RN REVIEW.
RP MEDLINE=97364701; PubMed=9218411;
RX Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RA "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -|- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -|- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT
CC LOWER LEVELS IN OTHER TISSUES.
CC -|- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D87559; BAA13419.1; -;
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation.
FT ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 392 AA; 43865 MW; 1DEACA2ADF4CEA8 CRC64;

Query Match 39.2%; Score 73; DB 1; Length 392;
Best Local Similarity 45.5%; Pred. No. 0.013;
Matches 15; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 5 KGDIDSNAAIDLSNKASLAFQKHLGKHLKDFDQ 37
DB 337 RGSLLDPYEGQETVVRAMLAFQKHLKEDYDQ 369

RESULT 8
ID PAF2_HUMAN STANDARD; PRT; 392 AA.
AC Q99487; O15458;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
GN PAF2H2.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase.";
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
RP TISSUE=Prostate;
RX MEDLINE=98161812; PubMed=9494101;
RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphee C.H.,
RA Moores K., Glover I.S., Tew D.G.;
RT "Expression, purification and characterization of a human
RT serine-dependent phospholipase A2 with high specificity for oxidized
RT phospholipids and platelet activating factor.";
RL Biochem. J. 330:1309-1315(1998).
RN [3]
RN REVIEW.
RP MEDLINE=97364701; PubMed=9218411;
RX Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RA "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -|- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -|- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,
CC 3,4-DICHLOROISOCOMARIN, DIISOPROPYL FLUOROPHOSPHATE (DFP) AND
CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -|- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT
CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO
CC AMYGDALA AND FRONTAL CORTEX.
CC -|- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D87845; BAA13468.1; -;
DR EMBL; U89386; AAC39707.1; -;
DR TM: 602344; -;
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation.
FT ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 L -> F (IN REF. 2).
SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;

Query Match 38.2%; Score 71; DB 1; Length 392;
Best Local Similarity 42.4%; Pred. No. 0.025;
Matches 14; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 5 KGDIDSNAAIDLSNKASLAFQKHLGKHLKDFDQ 37
DB 337 RGSLLDPYEGQETVVRAMLAFQKHLKEDYDQ 369

RESULT 8
ID PAF2_HUMAN STANDARD; PRT; 392 AA.
AC Q99487; O15458;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
GN PAF2H2.
OS Homo sapiens (Human).

RESULT	10
GFP3_ECOLI	
ID	GFP3_ECOLI STANDARD; PRT; 333 AA.
AC	P3398; P76094; P78062; P78291; Q03850; Q63208;
CD	01-FEB-1994 (Rel. 28, Created)
DT	20-AUG-2001 (Rel. 40, Last sequence update)
DDT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE C (EC 1.2.1.12) (GAPDH-C).
GN	GAPC OR B1416/B1417.
GS	Escherichia coli.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX	NCBI_TaxID=562;
RP	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=RIVER ISOLATE, AND CLINICAL ISOLATE;
RC	MEDLINE=98283700; PubMed=9622357;
RA	Espinosa-Urgel M., Koller R.;
RA	"Escherichia coli genes expressed preferentially in an aquatic
RT	environment";
RL	Mol. Microbiol. 28:325-332(1998).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	Hidalgo E., Limon A.; Aguilar J.;
RA	"A second Escherichia coli gene with similarity to gapA.";
RA	Microbiologia 12:99-106(1996).
RL	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12 / MG1655;
RC	MEDLINE=97426617; PubMed=9278503;
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mau B., Shao Y.;
RT	"The complete genome sequence of Escherichia coli K-12.";
RL	Science 277:1453-1474(1997).
RL	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RC	MEDLINE=97251357; PubMed=9097039;
RA	Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T,
RA	Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA	Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N,
RA	Sampegi K., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA	Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.;
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT	corresponding to the 28.0-40.1 min region on the linkage map.";
RL	DNA Res. 3:363-377(1996).
RL	[5]
RP	SEQUENCE OF 306-332 FROM N.A.
RC	STRAIN=K12;
RC	MEDLINE=92011371; PubMed=1917845;
RA	Hidalgo E., Chen Y.-M., Lin E.C.C., Aguilar J.;
RA	"Molecular cloning and DNA sequencing of the Escherichia coli K-12
RT	ald gene encoding aldehyde dehydrogenase.";
RL	J. Bacteriol. 173:6118-6123(1991).
RL	[6]
RP	SEQUENCE OF 1-13 FROM N.A.
RC	STRAIN=K12;
RC	MEDLINE=88232416; PubMed=2836696;
RA	Nakamura H., Murakami H., Yamato I., Anraku Y.;
RA	"Nucleotide sequence of the cybb gene encoding cytochrome b561 in
RT	Escherichia coli K12.";
RL	Mol. Gen. Genet. 212:1-5(1988).
RL	[7]
RP	SEQUENCE OF 1-165 FROM N.A.
RC	Krawetz S.;
RA	Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
RL	[8]

```
RP SEQUENCE OF 1-52 FROM N.A.
RX MEDLINE=87053179; PubMed=3780374;
RA Krawetz S.A., Connor W., Cannon P.D., Dixon G.H.;
RT "A vector-primer-cloner-sequencer plasmid for the construction of cDNA
RT libraries: evidence for a rat glyceraldehyde-3-phosphate
RT dehydrogenase-like mRNA and a ferritin mRNA within testis.";
RL DNA 5:427-435(1986).
CC -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
CC -!- CAUTION: IN THE K12 STRAIN THIS GENE IS DISRUPTED BY A STOP CODON
CC AND A FRAMESHIFT. IT SEEMS TO BE INTACT IN A NUMBER OF WILD
CC STRAINS.
CC -!- CAUTION: REF 8 AND REF 9 SEQUENCE WAS ORIGINALLY THOUGHT TO
CC ORIGINATE FROM RAT.
CC
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CC
CC EMBL: L09067; AAA23856.1; ALT_FRAME.
CC EMBL: AE000239; AAC74498.1; ALT_FRAME.
CC EMBL: AE000239; AAC74499.1; ALT_FRAME.
CC EMBL: D90780; BAA15033.1; ALT_FRAME.
CC EMBL: D90781; BAA15038.1; ALT_FRAME.
CC EMBL: M64541; -; NOT_ANNOTATED_CDS.
CC EMBL: X07569; -; NOT_ANNOTATED_CDS.
CC EMBL: X54798; CAA38569.1; -.
CC EMBL: M14166; AAA41178.1; -.
CC HSSP: F17721; LHGD.
CC EcoGene: EG12103; gapC.
CC InterPro: IPR000173; GAP_DH.
CC Pfam: PF00044; gpdh; 1.
CC PRINTS: PR00078; G3PDHGRNASE.
CC PROSITE: PS00071; G4PDH; 1.
KW Glycolysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
FT BINDING 150 150
FT ACT_SITE 177 177
FT (BY SIMILARITY).
FT ACTIVATES THIOL GROUP DURING CATALYSIS
FT (BY SIMILARITY).
FT CONFLICT 39 39 K -> Y (IN REF. 7 AND 8).
SQ SEQUENCE 333 AA; 35649 MW; E88223297376B0A0 CRC64;

Query Match 28.5%; Score 53; DB 1; Length 333;
Best Local Similarity 42.9%; Pred. No. 5.9;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLKLGKGDIDSNAAIDLSNKSALFLQKH 28
Db 20 LLEVKSNIDVAINDLTSPKILAYLLKH 47

RESULT 11
CSK1_SCHPO STANDARD; PRT; 306 AA.
AC P36615;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTEIN KINASE CSK1 (EC 2.7.1.-).
GN CSK1 OR SPAC104.06C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
```

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OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93223713; PubMed=8467814;
RA Molz L., Beach D.;
RT "Characterization of the fission yeast mcs2 cyclin and its associated
RT protein kinase activity.";
RL EMBO J. 12:1723-1732(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN. COULD FUNCTION IN ASSOCIATION WITH CYCLIN
CC MCS2.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDCX SUBFAMILY.
CC
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CC
CC EMBL: S59896; AAB26194.1; -.
CC EMBL: Z69239; CAA93215.1; -.
CC PIR: S39151; S39151.
CC HSSP: P24941; IAQ1.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_kin_actsite.
CC Pfam: PF00069; pkinase; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC TRANSFERASE: Serine/threonine-protein kinase; 1.
FT DOMAIN 11 306 PROTEIN KINASE.
FT NP_BIND 17 25 ATP (BY SIMILARITY).
FT BINDING 40 40 ATP (BY SIMILARITY).
FT ACT_SITE 129 129 BY SIMILARITY.
SQ SEQUENCE 306 AA; 34672 MW; E670D87547523D0C CRC64;

Query Match 27.4%; Score 51; DB 1; Length 306;
Best Local Similarity 40.7%; Pred. No. 10;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 IDSNAADLSNKSALFLQKHGLHKO 34
Db 103 IDTKCKIVLQISSALEVLEKHGILHRD 129

RESULT 12
FEMA_STAAU STANDARD; PRT; 433 AA.
AC P14304;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE FACTOR ESSENTIAL FOR EXPRESSION OF METHICILLIN RESISTANCE.
GN FEMA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=90136516; PubMed=2559314;
RA Berger-Baechi B., Barberis-Maino L., Straessle A., Kayser F.H.;
RT "Fema, a host-mediated factor essential for methicillin resistance in
RT Staphylococcus aureus: molecular cloning and characterization.";
```


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CC EMBL; J05571; AAA42106.1; -;
DR EMBL; AB000717; BAA19170.1; -;
DR EMBL; AB000716; BAA19170.1; JOINED.
DR PIR; A37118; A37118.
DR HSSP; P04384; IXRC.
DR InterPro; IPR002133; S-AdoMet_synt.
DR Pfam; PF00438; S-AdoMet_synt; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE.1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE.2; 1.
KW Transferase; One-carbon Metabolism; Multigene family; ATP-binding.
FT NP_BIND 131 136 ATP (POTENTIAL).
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43715 MW; 4DA9AFBF7D09C79 CRC64;

Query Match 27.2%; Score 50.5; DB 1; Length 395;
Best Local Similarity 41.0%; Pred. No. 16;
Matches 16; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

QY 1 MLKLGDISNAADLSNKASLAFLOKHLGL---HKDFD 36
| : | | | | | | | | | | | | | | | | | | | |
Db 64 MILLAGEITSRAIDYOKVVEAI--KHIGYDSSKGF 100

RESULT 15

SP21_YEAST STANDARD; PRT; 758 AA.
AC P35209;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE SPT21 PROTEIN.
GN SPT21 OR YMR179W OR YMR8010.09.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94186069; PubMed=8138180;
RA Natsoulis G., Winston F., Boeke J.D.;
RT "The SPT10 and SPT21 genes of Saccharomyces cerevisiae.";
RL Genetics 136:93-105(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR NORMAL TRANSCRIPTION AT A NUMBER OF LOCI IN YEAST.
CC

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DR EMBL; I24436; AAA35078.1; -;
DR EMBL; Z49808; CAA89912.1; -;
DR PIR; S47866; S47866.
DR SGD; S0004791; SPT21.
FT DOMAIN 127 144 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 672 682 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 758 AA; 84697 MW; 7DB3FCF7EE996705 CRC64;

Query Match 27.2%; Score 50.5; DB 1; Length 758;
Best Local Similarity 32.4%; Pred. No. 32;
Matches 11; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 3 KLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFD 36
| : | | | | | | | | | | | | | | | | | | | |
Db 475 KLEGDLDFNAEPPMSDFSDVVF-KDEMGWFSNEN 507

Search completed: March 9, 2002, 00:47:33
Job time: 794 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:33:04 ; Search time 94.88 seconds
(without alignments)
57.041 Million cell updates/sec

Title: US-09-922-067-1
Perfect score: 186
Sequence: 1 MLKLGDISNAADLSNKAFLQKHLGHRKFDQ 37

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	57	30.6	418	2 Q9X6T1	Q9X6T1 staphylococ
2	57	30.6	430	4 Q9HB15	Q9hb15 homo sapien
3	57	30.6	430	11 Q9ERS1	Q9ersi rattus norv
4	56	30.1	803	2 Q9FD70	Q9fd70 enterococcu
5	54	29.0	408	4 Q9HB14	Q9hb14 homo sapien
6	54	29.0	1089	9 Q9MCS3	Q9mcs3 bacterioph
7	54	29.0	1516	4 Q9C0D2	Q9c0d2 homo sapien
8	53.5	28.5	136	2 Q9AI05	Q9ai05 photorhabdu
9	53	28.5	56	2 Q57487	Q57487 caedibacter
10	53	28.5	111	2 Q9K5J8	Q9k5j8 bacillus an
11	53	28.5	238	9 Q9MET8	Q9met8 staphylococ
12	53	28.5	348	9 Q38045	Q38045 bacterioph
13	53	28.5	736	10 O80440	O80440 arabidopsis
14	53	28.5	1032	2 Q9KY11	Q9ky11 streptomyce
15	52.5	28.2	755	4 Q9UFE4	Q9ufe4 homo sapien
16	52	28.0	211	2 Q9AHD1	Q9ahd1 streptococc
17	52	28.0	422	2 P95734	P95734 staphylococ
18	52	28.0	803	1 Q9C4Z4	Q9c4z4 methanosarc
19	51	27.4	420	2 Q99UA7	Q99ua7 staphylococ

20	51	27.4	488	2 Q9K936	Q9k936 bacillus ha
21	51	27.4	660	10 Q40008	Q40008 hordeum vul
22	51	27.4	660	10 Q43482	Q43482 hordeum vul
23	51	27.4	2227	12 Q86775	Q86775 equine rhin
24	51	27.4	2247	12 Q39818	Q39818 equine rhin
25	51	27.4	2248	12 Q66774	Q66774 equine rhin
26	51	27.4	15281	3 Q09164	Q09164 tolypocladi
27	50.5	27.2	266	1 Q58769	Q58769 methanococc
28	50.5	27.2	395	11 Q99J57	Q99j57 mus musculu
29	50.5	27.2	727	2 Q65986	Q65986 clostridium
30	50.5	27.2	2285	2 Q31976	Q31976 bacillus su
31	50.5	27.2	2285	9 Q64046	Q64046 bacterioph
32	50	26.9	67	1 Q9HI99	Q9hi99 thermoplasm
33	50	26.9	115	2 Q9CEL2	Q9cel2 lactococcus
34	50	26.9	287	5 Q9W5X9	Q9w5x9 drosophila
35	50	26.9	413	5 Q25004	Q25004 homarus ame
36	50	26.9	609	5 Q94834	Q94834 trichomonas
37	49	26.3	285	10 Q49614	Q49614 arabidopsis
38	49	26.3	374	2 Q87702	Q87702 bacillus me
39	49	26.3	488	5 Q96693	Q96693 plasmodium
40	49	26.3	513	2 Q51545	Q51545 pseudomonas
41	49	26.3	558	2 Q9HTJ5	Q9htj5 pseudomonas
42	49	26.3	587	12 Q39279	Q39279 equine herp
43	49	26.3	652	5 Q93346	Q93346 caenorhabdi
44	49	26.3	683	11 P82198	P82198 mus musculu
45	49	26.3	862	10 Q9FT37	Q9ft37 taxus chine

ALIGNMENTS

RESULT 1
Q9X6T1
ID Q9X6T1 PRELIMINARY; PRT: 418 AA.
AC Q9X6T1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FACTOR ESSENTIAL FOR METHICILLIN RESISTANCE.
GN FEMA.
OS Staphylococcus warneri.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 20316;
RA Vannuffel P., Heusterspreute M., Gala J.-L.;
RT "Cloning and characterization of femA genes from Staphylococci
RT species";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144663; AAD33942.1; -;
DR InterPro; IPR003447; FemAB.
DR Pfam; PF02388; FemAB; 1.
SQ SEQUENCE 418 AA; 48703 MW; 62EA0F6DE50C5596 CRC64;

Query Match 30.6%; Score 57; DB 2; Length 418;
Best Local Similarity 48.5%; Pred. No. 6.8;
Matches 16; Conservative 0; Mismatches 13; Indels 4; Gaps 2;

QY 6 GDIDSNAAID--LSNKAFLQKHLGHRKFD 36
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 GDITGNAGNDWIFDKLASLGF--KHEGFHNGFD 150

RESULT 2
Q9HB15
ID Q9HB15 PRELIMINARY; PRT: 430 AA.
AC Q9HB15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE	ACETYL-COA ACETYLTTRANSFERASE/HMG-COA REDUCTASE.
GN	MVAE.
OS	Enterococcus faecalis (Streptococcus faecalis).
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC	Enterococcus.
OX	NCBI_TaxID=1351;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20353468; PubMed=10894743;
RR	Wilding E.I., Brown J.R., Bryant A.P., Chalker A.F., Holmes D.J.,
RT	Ingraham K.A., Iordanescu S., So C.Y., Rosenberg M., Gwynn M.N.;
RT	"Identification, evolution and essentiality of the mevalonate pathway
RT	for isopentenyl diphosphate biosynthesis in gram-positive cocci.";
RL	J. Bacteriol. 182:4319-4327(2000).
DR	EMBL; AF290092; AAC02439.1; -.
DR	InterPro; IPR002202; HMG-CoA_red.
DR	InterPro; IPR002155; Thiolase.
DR	Pfam; PF00368; HMG-CoA_red; 1.
DR	Pfam; PF00108; thiolase; 1.
DR	PRINTS; PR00071; HMGOARDTASE.
DR	PROSITE; PS50065; HMG_COA_REDUCTASE_4; 1.
DR	PROSITE; PS00098; THIOLASE_1; 1.
DR	Transferase.
KW	SEQUENCE 803 AA; 86496 MW; F3678A6E4AA43FC0 CRC64;
SQ	
Query Match 30.1%; Score 56; DB 2; Length 803;	
Best Local Similarity 28.6%; Pred. No. 20;	
Matches 10; Conservative 9; Mismatches 16; Indels 0; Gaps 0;	
QY	3 KLKGDIDSNAADLSNKASIAFLQKLGLHKHDFDQ 37 I : : : : : I : : : : : I :
Db	16 KYGSLSQSVSAVDLGTHTVTTQLLKRUHSTISEIDQ 50 I : : : : : I : : : : : I :
RESULT	5
Q9HB14	PRELIMINARY; PRT; 408 AA.
ID	O9HB14;
DC	A.
AT	01-WAR-2001 (TREMBLrel. 16, Created)
DT	01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	TANDEM PORE DOMAIN POTASSIUM CHANNEL THIK-1.
GN	KCNK13.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Rajan S., Derst C.;
RT	"Cloning and sequencing of two novel tandem pore domain potassium
RT	channels.";
RL	J. Biol. Chem. 0:0-0(2001).;
DR	EMBL; AF287303; AAG32314.1; -.
DR	InterPro; IPR003280; 2porek_channel.
DR	InterPro; IPR001622; Channel_pore_k.
DR	PRINTS; PRO1333; 2PORECHANNEL.
DR	Ionic channel.
KW	SEQUENCE 408 AA; 45392 MW; B7E3CA1AFD59E419 CRC64;
SQ	
Query Match 29.0%; Score 54; DB 4; Length 408;	
Best Local Similarity 48.1%; Pred. No. 18;	
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;	
QY	3 KLKGDIDSNAADLSNKASIAFLQKHIL 29 I : : : : : I : : : : : I I I I I
Db	341 RLSEGMTSMKDLLANKASIAFLQKQL 367 I : : : : : I : : : : : I I I I I
RESULT	6
Q9MCS3	


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ID Q9MCS3 PRELIMINARY; PRT; 1089 AA.
AC
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE TAIL LENGTH TAPE MEASURE PROTEIN.
GN H.
OS Bacteriophage HK97.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=37554;
RN [1]
RP SEQUENCE FROM N.A.
RA Juharia R., Ford M.E., Duda R.L., Youton A., Hatfull G.F.,
RA Hendrix R.W.;
RT "Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic
RT mosaicism in the lambdaoid bacteriophages."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF069529; AAF31092.1; -
SQ SEQUENCE 1089 AA; 116230 MW; 2B425B4C30EF6C1D CRC64;

Query Match 29.0%; Score 54; DB 9; Length 1089;
Best Local Similarity 29.6%; Pred. No. 54;
Matches 16; Conservative 9; Mismatches 11; Indels 18; Gaps 2;

QY 2 LKLGDI-----DSNAAIDLSNKASL-----AFLOKHLGLHKDFDQ 37
Db 752 VKLKGQLRYEANIADSNASARAANEALGLGYGQTRFRERLQEQFNLRKEFEQ 805

RESULT 7
Q9C0D2 PRELIMINARY; PRT; 1516 AA.
AC Q9C0D2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE KIAA1731 PROTEIN (FRAGMENT).
GN KIAA1731.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:347-355(2000).
DR EMBL; AB051518; BAB21822.1; -
FT NON_TER 1
SQ SEQUENCE 1516 AA; 171062 MW; 26FE7721B28F2D02 CRC64;

Query Match 29.0%; Score 54; DB 4; Length 1516;
Best Local Similarity 42.9%; Pred. No. 78;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 KGDIDSNAAIDLSNKASLAFLOKHLGLH 32
Db 624 KGLVSCSDIPTSQDGLSLFQQFLPLH 651

RESULT 8
Q9AI05 PRELIMINARY; PRT; 136 AA.
ID Q9AI05
AC Q9AI05;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

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```

DE YBAB.
GN YBAB.
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NC19, ATCC29304;
RA Cliche T.A., Bintrim S.B., Horswill A.R., Ensign J.C.;
RT "A phosphopantetheinyl transferase homolog is essential for
RT photorhabdus luminescens to support the growth and reproduction of the
RT entomopathogenic nematode Heterorhabditis bacteriophora."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288081; AAK16080.1; -
SQ SEQUENCE 136 AA; 15987 MW; FBE5FCD757D28284 CRC64;

Query Match 28.8%; Score 53.5; DB 2; Length 136;
Best Local Similarity 31.9%; Pred. No. 5.9;
Matches 15; Conservative 6; Mismatches 7; Indels 19; Gaps 2;

QY 8 IDSNAADLSNKA-SLAFLOKHLGL-----HKDF 35
Db 73 VDADEHIDIVNKRSLDEIQPHLGIEIKSFELIDDIDKFTFDHKDF 119

RESULT 9
Q57487 PRELIMINARY; PRT; 56 AA.
ID Q57487
AC Q57487;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE REBC.
GN REBC.
OS Caedibacter taeniospiralis.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsia group ciliate endosymbionts; Caedibacter.
OX NCBI_TaxID=28907;
RN [1]
RP SEQUENCE FROM N.A.
RA Heruth D.P., Pond F.R., Diltz J.A., Quackenbush R.L.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04524; AAA73410.1; -
DR EMBL; U04523; AAA73406.1; -
SQ SEQUENCE 56 AA; 6081 MW; 1910AA106C5363A7 CRC64;

Query Match 28.5%; Score 53; DB 2; Length 56;
Best Local Similarity 27.8%; Pred. No. 2.5;
Matches 10; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 MLKLGDIIDSNAAIDLSNKASLAFLOKHLGLHKDF 36
Db 15 MMDPKNNVASOGAYDIVSMAAASAVQNELAMHSGE 50

RESULT 10
Q9K5J8 PRELIMINARY; PRT; 111 AA.
ID Q9K5J8
AC Q9K5J8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RSBV PROTEIN.
GN RSBV.
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1392;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=90236919; PubMed=2139648;
RA Ye Z.H., Buranen S.L., Lee C.Y.;
RT "sequence analysis and comparison of int and xls genes from
RT staphylococcal bacteriophages L54a and phi 11.";
RL J. Bacteriol. 172:2568-2575(1990).
DR EMBL: M34832; AAA32198.1; -
DR InterPro: IPR002104; Phage_integrate.
DR Pfam: PF00589; Phage_integrate; 1.
SQ SEQUENCE 348 AA; 41378 MW; E35C7CB6E70FD26 CRC64;

Query Match 28.5%; Score 53; DB 9; Length 348;
Best Local Similarity 58.8%; Pred. No. 20;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
QY      3 KLKGDIDSNAAIDLSNK 19
        1:1:1:1 | 1:1:1:
Db      209 KIKGEIDVKKINLSNR 225
```

```

RESULT 13
O80440 PRELIMINARY; PRT; 736 AA.
ID
O80440;
AC
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE F16M14.8 PROTEIN.
DE F16M14.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RX
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RA "Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC003028; AAC27164.1; -.
DR
SO SEQUENCE 736 AA; 83645 MW; 959791363387326 CRC64;

```

```

Query Match      28.5%;   Score 53;   DB 10;   Length 736;
Best Local Similarity 54.5%;   Pred. No. 48;
Matches 12;   Conservative 4;   Mismatches 6;   Indels 0;   Gaps 0

```

RESULT 14
Q9KYL1
ID Q9KYL1
PRELIMINARY: P

RESULT	14
ID	Q9KYL1
Q9KYL1	PRELIMINARY; PRT; 1032 AA.
AC	O9KYL1;
DC	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE	HYPOTHETICAL 113.7 KDA PROTEIN.
OS	SC1G8. 02C.
OS	Streptomyces coelicolor.
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC	Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces
OX	NCBI_TaxID=1902;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	
RC	STRAIN=A3(2);
RA	Saunders D.C.; Harris D.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=970003351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RT Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL356593; CAB92219.1; -;
KW Hypothetical protein.
SQ SEQUENCE 1032 AA; 113651 MW; 4EF959BB8BCDEF21 CRC64;

Query Match 28.5%; Score 53; DB 2; Length 1032;
Best Local Similarity 44.0%; Pred. No. 70;
Matches 11; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 9 DSNAAIDLSNKAFLQKHLGLHK 33
DB 685 DQLPLDLSERAHLALRAHLDTHE 709

RESULT 15

Q9UFE4 PRELIMINARY; PRT; 755 AA.
AC Q9UFE4;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
DE HYPOTHETICAL 88.2 KDA PROTEIN.
GN DKFZP434A128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL12120; CAB59277.1; -;
KW Hypothetical protein.
SQ SEQUENCE 755 AA; 88230 MW; B971EE2F7E0F958B CRC64;

Query Match 28.2%; Score 52.5; DB 4; Length 755;
Best Local Similarity 28.6%; Pred. No. 58;
Matches 14; Conservative 10; Mismatches 12; Indels 13; Gaps 2;

QY 1 MLKLGIDISNAADLSN-----KASLAFLQKHLGLHKDFDQ 37
DB 318 MQRDGDID-NCALELARIKETREKENLYNKEIKFLEISEIGNTEFEK 365

Search completed: March 9, 2002, 00:46:48
Job time: 824 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:56 ; Search time 114.5 Seconds
(without alignments)
19.408 Million cell updates/sec

Title: US-09-922-067-2

Perfect score: 170

Sequence: 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

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16: /SID22/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq/AA1997.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq/AA2001.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	170	100.0	440	22	AAE00782 Mouse-Human plasma
2	170	100.0	440	22	AAE00783 Mouse-Human plasma
3	170	100.0	441	16	AAE00784 Human acetyl hydro
4	170	100.0	441	16	AAE00785 Human acetyl hydro
5	170	100.0	441	16	AAE00786 Human acetyl hydro
6	170	100.0	441	16	AAE00787 Human acetyl hydro
7	170	100.0	441	16	AAE00788 Human acetyl hydro
8	170	100.0	441	16	AAE00789 Human acetyl hydro
9	170	100.0	441	16	AAE00790 Human acetyl hydro
10	170	100.0	441	16	AAE00791 Human acetyl hydro
11	170	100.0	441	16	AAE00792 Human acetyl hydro

12	170	100.0	441	16	AAE00782	Human acetyl hydro
13	170	100.0	441	16	AAE00783	Human acetyl hydro
14	170	100.0	441	16	AAE00784	Human plasma plate
15	170	100.0	441	18	AAE00785	Human platelet-act
16	170	100.0	441	18	AAE00786	Human plasma plate
17	170	100.0	441	18	AAE00787	Platelet-activatin
18	170	100.0	441	19	AAE00788	Human plasma plate
19	170	100.0	441	20	AAE00789	Human plasma plate
20	170	100.0	441	20	AAE00790	Human PAF-AH prote
21	170	100.0	441	21	AAE00791	Plasma platelet-ac
22	170	100.0	441	21	AAE00792	Human low density
23	170	100.0	441	21	AAE00793	Human platelet-act
24	170	100.0	441	21	AAE00794	Human PAF-AH prote
25	170	100.0	441	22	AAE00795	Human plasma plate
26	170	100.0	441	22	AAE00796	Human plasma plate
27	170	100.0	441	22	AAE00797	Human plasma plate
28	170	100.0	441	22	AAE00798	Human plasma plate
29	170	100.0	441	22	AAE00799	Human plasma plate
30	170	100.0	441	22	AAE00799	Human plasma plate
31	170	100.0	441	22	AAE00799	Human plasma plate
32	170	100.0	441	22	AAE00799	Human plasma plate
33	170	100.0	441	22	AAE00799	Human platelet-act
34	170	100.0	441	22	AAE00799	Human plasma plate
35	170	100.0	441	22	AAE00799	Human plasma plate
36	170	100.0	441	22	AAE00799	Human plasma plate
37	170	100.0	441	22	AAE00799	Human plasma plate
38	170	100.0	441	22	AAE00799	Human plasma plate
39	170	100.0	441	22	AAE00799	Platelet-activatin
40	170	100.0	441	22	AAE00799	Human T-cell lymph
41	162	95.3	441	22	AAE00799	Human plasma plate
42	155	91.2	444	18	AAE00799	Bovine platelet-act
43	155	91.2	444	20	AAE00799	Bovine plasma plat
44	155	91.2	444	20	AAE00799	Bovine PAF-AH prot
45	155	91.2	444	21	AAE00799	A bovine platelet-

ALIGNMENTS

RESULT 1

AAE00782 AAE00782 standard; Protein; 440 AA.

AC AAE00782;

XX

XX

DT 02-JUL-2001 (first entry)

XX

DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHCl.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;

KW antinflammatory; septicaemia; inflammation; haemostasis; parturition;

KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX

EH Key Location/Qualifiers

FT Region

FT /note= "Corresponds to N-terminal 97 amino acids of mouse plasma platelet-activating factor acetylhydrolase (PAF-AH)"

FT 98..440

FT Region

FT /note= "Corresponds to C-terminal 343 amino acids of human plasma platelet-activating factor acetylhydrolase (PAF-AH)"

FT US6203790-B1.

XX

XX 20-MAR-2001.

XX

XX 23-MAY-2000; 2000US-0577758.

XX

XX 07-JUN-1995; 95US-0480658.

PR

PR 22-JAN-1998; 98US-0010715.
 PR 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0318905.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX
 XX WPI: 2001-280610/29.
 DR N-PSDB; AAD04168.
 DR
 XX
 PT Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF -
 XX
 XX Example 8; Column -: 54pp; English.
 PS
 XX The present sequence is mouse-human plasma platelet-activating factor
 XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHC1.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 XX Sequence 440 AA;
 SQ
 Query Match 100.0%; Score 170; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 |||||
 Db 297 wmfplgdevysripqplffinsefyqpan 326
 RESULT 2
 AAE00783
 ID AAE00783 standard; Protein; 440 AA.
 XX
 AC AAE00783;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.
 DE
 XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antinflammatory; septicemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 1..40
 FT /note= "Corresponds to N-terminal 40 amino acids of mouse
 FT plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 FT 41..440
 FT Region
 FT /note= "Corresponds to C-terminal 400 amino acids of

FT human plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)*
 XX
 PN US6203790-B1.
 XX
 PD 20-MAR-2001.
 XX
 XX 23-MAY-2000; 2000US-0577758.
 PF
 XX 07-JUN-1995; 95US-0480658.
 PR 22-JAN-1998; 98US-0010715.
 PR 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0318905.
 XX
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 PI
 XX WPI: 2001-280610/29.
 DR N-PSDB; AAD04169.
 DR
 XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF -
 XX
 XX Example 8; Column -: 54pp; English.
 PS
 XX The present sequence is mouse-human plasma platelet-activating factor
 XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHC2.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 XX Sequence 440 AA;
 SQ
 Query Match 100.0%; Score 170; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 5.4e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 |||||
 Db 297 wmfplgdevysripqplffinsefyqpan 326
 RESULT 3
 AAR73048
 ID AAR73048 standard; Protein; 441 AA.
 XX
 AC AAR73048;
 XX
 DT 06-DEC-1995 (first entry)
 XX
 XX Human acetyl hydrolase (AH) mutant C291S.
 DE
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; Inflammatory;
 KW disease; pleurisy; diagnosis.
 KW
 XX Homo sapiens.
 OS

```

XX Key Location/Qualifiers
FH Misc-difference 291
FT /note= "Wild-type Cys is substd. by Ser."
XX
XX
XX WO9509921-A.
XX PD 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX
XX Example 10; ; 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AAO87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
XX in the patent specification; they have been derived from the original
XX wild-type protein (AAR71913).
XX
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
Db |||||
298 wmfplgdevysripqplffinsefyqpan 327

RESULT 4
AAR73049
ID AAR73049 standard; Protein; 441 AA.
XX
XX AAR73049;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C334S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 334
FT /note= "Wild-type Cys is substd. by Ser."
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX

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XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
XX acetyl:hydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy
XX
XX Example 10; ; 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AAO87947) has been isolated and
XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX made with single amino acid changes for the purposes of identifying
XX the active site of AH. The sequences of these mutants are not given
XX in the patent specification; they have been derived from the original
XX wild-type protein (AAR71913).
XX
XX The AH gene and its product are useful in the treatment of inflammatory
XX diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX gene may also be used in raising monoclonal antibodies specific for AH
XX that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
Db |||||
298 wmfplgdevysripqplffinsefyqpan 327

RESULT 5
AAR73050
ID AAR73050 standard; Protein; 441 AA.
XX
XX AAR73050;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C407S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 407
FT /note= "Wild-type Cys is substd. by Ser."
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX Wilder CL;
XX
XX WPI; 1995-155262/20.
XX

```

PT New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
XX inflammatory diseases, e.g. pleurisy

PS Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
Db ||||||||||||||||||||||||||||||||
298 wmfplgdevysripqplffinsefyqypan 327

RESULT 6

AAR71920
ID AAR71920 standard; Protein; 441 AA.

XX AAR71920;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant S108A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given

CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
Db ||||||||||||||||||||||||||||||||
298 wmfplgdevysripqplffinsefyqypan 327

RESULT 7

AAR71921
ID AAR71921 standard; Protein; 441 AA.

XX AAR71921;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant S273A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
 |||||
 Db 298 wmfplgdevysripqplffinseyfqpypan 327

RESULT 8

AAR71922
 ID AAR71922 standard; Protein: 441 AA.

XX AC AAR71922;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant D296A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 296 /note= "Wild-type Asp is substd. by Ala."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX DR WPI: 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,
 PT acetyl hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
 |||||
 Db 298 wmfplgdevysripqplffinseyfqpypan 327

RESULT 9

Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

AAR71923

ID AAR71923 standard; Protein: 441 AA.

XX AC AAR71923;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D338A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 338 /note= "Wild-type Asp is substd. by Ala."

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX DR WPI: 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,
 PT acetyl hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; ; 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
 |||||
 Db 298 wmfplgdevysripqplffinseyfqpypan 327

RESULT 10

AAR71924
 ID AAR71924 standard; Protein: 441 AA.

XX AC AAR71924;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant H351A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

KW disease; pleurisy; diagnosis.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 351
 FT /note= "Wild-type His is substd. by Ala."
 XX
 PN W09509921-A.
 XX
 XX 13-APR-1995.
 PD
 PF 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 PI
 XX WPI; 1995-155262/20.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 PT
 XX Example 10; ; 88pp; English.
 PS
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. NO. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 DB ||||||||||||||||||||||||||||
 298 wmfplgdevysripplffinsefygpan 327
 RESULT 11
 AAR71925
 ID AAR71925 standard; Protein; 441 AA.
 XX
 AC AAR71925;
 XX
 XX 06-DEC-1995 (first entry)
 DT
 XX Human acetyl hydrolase (AH) mutant H395A/H399A.
 DE
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 395
 FT /note= "Wild-type His is substd. by Ala."
 FT 399
 FT /note= "Wild-type His is substd. by Ala."
 FT
 XX

PN W09509921-A.
 XX
 XX 13-APR-1995.
 PD
 PF 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 PI
 XX WPI; 1995-155262/20.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 PT
 XX Example 10; ; 88pp; English.
 PS
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. NO. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 DB ||||||||||||||||||||||||||||
 298 wmfplgdevysripplffinsefygpan 327
 RESULT 12
 AAR73046
 ID AAR73046 standard; Protein; 441 AA.
 XX
 AC AAR73046;
 XX
 XX 06-DEC-1995 (first entry)
 DT
 XX Human acetyl hydrolase (AH) mutant C67S.
 DE
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 67
 FT /note= "Wild-type Cys is substd. by Ser."
 FT
 PN W09509921-A.
 XX
 XX 13-APR-1995.
 PD
 PF 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 PI
 XX WPI; 1995-155262/20.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 PT
 XX Example 10; ; 88pp; English.
 PS
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. NO. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 DB ||||||||||||||||||||||||||||
 298 wmfplgdevysripplffinsefygpan 327

PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Example 10; ; 88pp; English.
 XX
 CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFYQYAN 30
 Db 298 wmfplgdevysripqplffinsefyqypan 327
 RESULT 13
 AAR73047
 ID AAR73047 standard; Protein; 441 AA.
 AC AAR73047;
 XX
 XX 06-DEC-1995 (first entry)
 DE Human acetyl hydrolase (AH) mutant C229S.
 XX
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 229
 FT /note= "Wild-type Cys is substd. by Ser."
 XX
 XX W09509921-A.
 PN
 XX 13-APR-1995.
 PD
 XX 06-OCT-1994; 94WO-US11340.
 PF
 XX 06-OCT-1993; 93US-0133803.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Example 10; ; 88pp; English.

XX
 CC The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WMFPLGDEVYSRIPOPLFFINSEYFYQYAN 30
 Db 298 wmfplgdevysripqplffinsefyqypan 327
 RESULT 14
 AAR71913
 ID AAR71913 standard; Protein; 441 AA.
 XX
 XX AAR71913;
 AC
 XX 05-DEC-1995 (first entry)
 DT
 DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
 XX
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX W09509921-A.
 PN
 XX 13-APR-1995.
 PD
 XX 06-OCT-1994; 94WO-US11340.
 PF
 XX 06-OCT-1993; 93US-0133803.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 DR
 XX N-PSDB; AAQ87947.
 DR
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Claim 5; Page 53-54; 88pp; English.
 PS
 CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
 CC is useful in the treatment of inflammatory diseases, in particular
 CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
 CC raising monoclonal antibodies specific for PAF-AH that are useful in
 CC the diagnosis of such diseases.
 XX
 SQ Sequence 441 AA;
 Query Match 100.0%; Score 170; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Search completed: March 9, 2002, 00:31:57
Job time: 443 sec

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMPPLGDEVYSRIPQPLFFINSEYFOYPAN 30
|||||
Db 298 wmfplgdevysripqplffinsefyqypan 327

RESULT 15

AAW26498
ID AAW26498 standard; Protein: 441 AA.

XX
AC AAW26498;

XX
DT 05-JAN-1998 (first entry)

XX
DE Human platelet-activating factor acetylhydrolase.

XX
KW Platelet-activating factor acetylhydrolase; PAF-AH; human;
inflammation; asthma; pleurisy; necrotising enterocolitis;
XX
KW adult respiratory distress syndrome; therapy.

XX
OS Homo sapiens.

XX
PN US5656431-A.

XX
PD 12-AUG-1997.

XX
PF 06-OCT-1993; 93US-0133803.

XX
PR 07-JUN-1995; 95US-0483232.

XX
PR 06-OCT-1993; 93US-0133803.

XX
PR 06-OCT-1994; 94US-0318905.

XX
PA (ICOS-) ICOS CORP.

XX
PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX
PI Wilder CL;

XX
DR WPI; 1997-414580/38.

XX
DR N-PSDB; AAT87048.

XX
PT Detecting lesions in human platelet-activating factor

XX
PT acetylhydrolase gene - by comparison with defined wild-type gene

XX
PT sequence

XX
PS Example 3; Column 47-50; 53pp; English.

XX
CC This polypeptide comprises human plasma platelet-activating factor
acetylhydrolase (PAF-AH), a protein that inactivates PAF and
inactivates oxidatively fragmented phospholipids such as products of
the arachidonic acid cascade that mediate inflammation. Its
sequence was deduced from a full-length cDNA clone (see AAT87048)
obtained from a macrophage cDNA library. Mouse, dog, cattle,
chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have
also been identified. Recombinant PAF-AH polypeptides can be
produced in prokaryotic or eukaryotic host cells and used to mimic
or augment normal processes of resolution of inflammation in vivo.
Examples describe the in vivo therapeutic effect of recombinant
PAF-AH products on acute inflammation, pleurisy, asthma,
necrotising enterocolitis and adult respiratory distress syndrome
in animal models.

XX
SQ Sequence 441 AA;

Query Match 100.0%; Score 170; DB 18; Length 441;

Best Local Similarity 100.0%; Pred. No. 5,5e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WMPPLGDEVYSRIPQPLFFINSEYFOYPAN 30

|||||

Db 298 wmfplgdevysripqplffinsefyqypan 327

us-09-922-067-2.rag

• Mon Mar 11 10:01:59 2002

Query Match 100.0%; Score 170; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
|||||
DB 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

RESULT 2

US-08-387-858A-2
; Sequence 2, Application US/08387858A
; Patent No. 5981252
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 24 February 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994

ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-387-858A-2

Query Match 100.0%; Score 170; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
|||||
DB 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

RESULT 3

US-09-294-384B-2

; Sequence 2, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,384B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858
FILING DATE: 24 February 1995
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994

ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-09-294-384B-2

Query Match 100.0%; Score 170; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
|||||
DB 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30

RESULT 4

US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl


```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/318,905
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/133,803
: FILING DATE: 6-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5641669and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 32205
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3658
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 441 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-318-905-8
:
: Query Match 100.0%; Score 170; DB 1; Length 441;
: Best Local Similarity 100.0%; Pred. No. 4.4e-13;
: Matches 30; Conservative 0; Mismatches 0; Indels
:
: QY 1 WMFPLGDEVYSRIPQPLFFINSEFYQYPAN 30
: | | | | | | | | | | | | | | | | | | | |
: DB 298 WMFPLGDEVYSRIPQPLFFINSEFYQYPAN 327
:
: RESULT 6
: US-08-483-232-8
: Sequence 8, Application US/08483232
: Patent No. 5656431
: GENERAL INFORMATION:
: APPLICANT: Cousens, Lawrence S.
: APPLICANT: Eberhardt, Christine D.
: APPLICANT: Gray, Patrick W.
: APPLICANT: Le Trong, Hal
: APPLICANT: Tjoelker, Larry W.
: APPLICANT: Wilder, Cheryl L.
: TITLE OF INVENTION: platelet-Activating Factor
: TITLE OF INVENTION: Acetylhydrolase
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/483,232
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/318,905
: FILING DATE: 06-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/133,803
: FILING DATE: 06-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5656431and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/32689

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-232-8

Query Match 100.0%; Score 170; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
|||||
DB 298 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 327

RESULT 7
US-08-483-140-8
Sequence 8, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-8

Query Match 100.0%; Score 170; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
|||||
DB 298 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 327

RESULT 8
US-08-485-938A-8
Sequence 8, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-8

Query Match 100.0%; Score 170; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
|||||
DB 298 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 327

RESULT 9
US-08-910-041-8
Sequence 8, Application US/08910041
Patent No. 5977308
GENERAL INFORMATION:

APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-041-8

Query Match 100.0%; Score 170; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
Db 298 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 327

RESULT 10
US-09-328-474-8
Sequence 8, Application US/09328474
Patent No. 6045794
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,474
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-328-474-8

Query Match 100.0%; Score 170; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
Db 298 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 327

RESULT 11
US-09-100-546-8
Sequence 8, Application US/09100546
Patent No. 6099836
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 100.0%; Score 170; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WMFPLGDEVYSRIPQLFFINSEYQYPAN 30
|||||
Db 298 WMFPLGDEVYSRIPQLFFINSEYQYPAN 327

RESULT 12
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 100.0%; Score 170; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WMFPLGDEVYSRIPQLFFINSEYQYPAN 30
|||||
Db 298 WMFPLGDEVYSRIPQLFFINSEYQYPAN 327

RESULT 13
US-09-577-758-8
Sequence 8, Application US/09577758
Patent No. 6203790
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,758
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/010,715
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6203790and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:

US-08-485-938A-33

QY 1 WMEPLGDEVYSRIPQPPLFFINSEYFQYPAN 30
 || || | : ||| ||| ||| ||| : || |
Dh 299 WMLPLDDAIYSRIPQPPLFFINSERFOFPEN 328

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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:07 ; Search time 53.53 Seconds
(without alignments)
42.691 Million cell updates/sec

Title: US-09-922-067-2

Perfect score: 170
Sequence: 1 WMFPLGDEVYSRIPQLFFINSEYFQYPAN 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	100.0	441	2 S60247	platelet-activating
2	128	75.3	436	2 JC5021	platelet-activating
3	57	33.5	384	2 T32756	hypothetical prote
4	53	31.2	476	2 T28936	hypothetical prote
5	52	30.6	215	2 F71101	hypothetical prote
6	52	30.6	760	2 S64023	ALK1 protein - yea
7	52	30.6	1038	2 JC6027	115K outer membran
8	51	30.0	182	2 T06198	lipoygenase (EC 1
9	51	30.0	313	2 T11153	NADH dehydrogenase
10	51	30.0	862	2 T05941	lipoygenase (EC 1
11	50.5	29.7	835	2 S63463	hypothetical prote
12	50.5	29.7	920	2 S63687	endo-alpha-sialida
13	49.5	29.1	583	2 B82744	conserved hypothet
14	49.5	29.1	1658	2 T42642	phosphoinositide 3
15	49	28.8	299	2 S73452	protein trsb - Myc
16	49	28.8	399	2 S68805	pectin acetylster
17	49	28.8	489	2 C75269	hypothetical prote
18	49	28.8	600	2 E86854	hypothetical prote
19	49	28.8	735	2 D86465	probable integral
20	48.5	28.5	91	2 T17521	hypothetical prote
21	48.5	28.5	828	2 S34695	hypothetical prote
22	48	28.2	216	2 G85642	hypothetical prote
23	48	28.2	266	2 S73887	MG133 homolog A65
24	48	28.2	546	2 C56976	transfer complex p
25	48	28.2	690	2 T27357	hypothetical prote
26	48	28.2	726	2 T35865	probable cyclase -
27	47.5	27.9	1063	2 T38732	probable helicase
28	47.5	27.9	1155	2 E92144	transcription-repa
29	47	27.6	448	1 B42022	transcription fact

30 47 27.6 503 2 B83437
31 47 27.6 558 2 T47508
32 47 27.6 692 1 P3XRPC
33 47 27.6 706 2 T08313
34 47 27.6 754 2 S52816
35 47 27.6 1155 2 S64365
36 46 27.1 667 2 T41306
37 46 27.1 759 2 B82919
38 46 27.1 804 2 S64090
39 45.5 26.8 142 2 T27965
40 45.5 26.8 335 2 B71361
41 45.5 26.8 399 2 E84955
42 45.5 26.8 941 2 S78633
43 45 26.5 152 1 ZDBPG4
44 45 26.5 435 2 B86149
45 45 26.5 794 2 T52441

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schlimpf, W

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g780133

Query Match 100.0%; Score 170; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 4.5e-17;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPQLFFINSEYFQYPAN 30

|||||

Db 298 WMFPLGDEVYSRIPQLFFINSEYFQYPAN 327

RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C>Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KAR1>

A:Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAAL1054.1; PID:g1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>

F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      30.6%; Score 52; DB 2; Length 215;
Best Local Similarity 42.9%; Pred. No. 3.5;
Matches 12; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
```

A:Reference number: S64003
A:Accession: S64023
A:Molecule type: DNA
A:Residues: 1-760 <HEB>
A:Cross-references: NID:g1322486; PIDN:CAA96721.1; PID:g24385
A:Experimental source: strain S288C
R:Rognes, T.
submitted to the EMBL Data Library, May 1995
A:Reference number: S57396
A:Accession: S57396
A:Molecule type: DNA
A:Residues: 1-757, 'AL', <ROG>
A:Cross-references: EMBL:X87672; NID:g861109; PIDN:CAA61012.1; PID:g861110
C:Genetics:
A:Gene: SGD:ALK1
A:Cross-references: SGD:S0002989; MIPS:YGL021W
A:Map position: 7L

RESULT 7
JC6027
115K outer membrane protein precursor - Bacteroides thetaiotaomicron
N:Alternate names: Susc protein
C:Species: Bacteroides thetaiotaomicron

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: JC6027
R;Reeves, A.R.; D'Elia, J.N.; Frias, J.; Salyers, A.A.
J. Bacteriol. 178, 823-830, 1996

A;Title: A Bacteroides thetaiotaomicron outer membrane protein that is essential for utilization of cellobiose

A;Reference number: JC6027; MUID:96146534

A;Accession: JC6027

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-1038 <R>

A;Cross-references: GB:L49338; NID:g1100064; PIDN:AAA95938.1; PID:g1100065

A;Note: It is uncertain whether Met-1, Met-14 or Met-20 is the initiator
C;Comment: This protein is an integral outer membrane protein, and it is essential for utilization of cellobiose

C;Genetics:

A;Gene: susC

C;Keywords: transmembrane protein

F;1-39/Domain: signal sequence #status predicted <SIG>

F;40-1038/Product: 115K outer membrane protein #status predicted <MAT>

F;1028-1038/Domain: transmembrane #status predicted <TM>

Query Match 30.6%; Score 52; DB 2; Length 1038;

Best Local Similarity 61.5%; Pred. No. 22;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 PLFFINSEYFQYP 28

||: |||||

Db 664 PLYVNVNEYAQP 676

RESULT 8

T06198

lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)

C;Species: Hordeum vulgare (barley)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C;Accession: T06198

R;Rouster, J.; Leah, R.; Mundy, J.; Cameron-Mills, V.

Plant J. 11, 513-523, 1997

A;Title: Identification of a methyl jasmonate-responsive region in the promoter of a lipid transfer protein

A;Reference number: 215527; MUID:97260963

A;Accession: T06198

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-182 <R>

A;Cross-references: EMBL:U83904; NID:g1814015; PIDN:AAB41791.1; PID:g1814016

C;Genetics:

A;Gene: Lox1

A;introns: 65/1; 163/3

C;Superfamily: lipoxigenase

C;Keywords: oxidoreductase

Query Match 30.0%; Score 51; DB 2; Length 182;

Best Local Similarity 38.7%; Pred. No. 4;

Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYF--QYPA 29

||: |||||

Db 146 WIYPAANYRSRV----FFANDTLPQMPA 172

RESULT 9

T11153

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - hardbacked tick (Rhodospirillum rubrum)

C;Species: Rhodospirillum rubrum

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000

C;Accession: T11153

R;Black IV, W.C.; Roehrdanz, R.L.

Mol. Biol. Evol. 15, 1772-1785, 1998

A;Title: Mitochondrial gene order is not conserved in arthropods: prostriate and metastriate orders

A;Reference number: 217252; MUID:99083443

A;Accession: T11153

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-313 <BLA>

A;Cross-references: EMBL:AF081829; NID:g4164556; PID:g4164557; PIDN:AAD05517.1

C;Genetics:

A;Gene: mitochondrial

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 30.0%; Score 51; DB 2; Length 313;

Best Local Similarity 66.7%; Pred. No. 7.6;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 YSRIPQPLFFINSEY 24

||: |||||

Db 270 YLRILTPLEFINSKF 284

RESULT 10

T05941

lipoxigenase (EC 1.13.11.12) 1 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C;Accession: T05941

R;van Mechelen, J.R.; Smits, M.; Douma, A.C.; Rouster, J.; Cameron-Mills, V.; Heidekamp

Biochim. Biophys. Acta 1254, 221-225, 1995

A;Title: Primary structure of a lipoxigenase from barley grain as deduced from its cDNA

A;Reference number: 215463; MUID:95127754

A;Accession: T05941

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-862 <VAN>

A;Cross-references: EMBL:L35931; NID:g532571; PIDN:AAA64893.1; PID:g532572

C;Genetics:

A;Gene: LoxA

C;Superfamily: lipoxigenase

C;Keywords: oxidoreductase

Query Match 30.0%; Score 51; DB 2; Length 862;

Best Local Similarity 38.7%; Pred. No. 25;

Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

QY 1 WMFPLGDEVYSRIPQPLFFINSEYF--QYPA 29

||: |||||

Db 146 WIYPAANYRSRV----FFANDTLPQMPA 172

RESULT 11

S63463

hypothetical protein YPL019c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein LPB12c

C;Species: Saccharomyces cerevisiae

C;Date: 16-May-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999

C;Accession: S63463

R;Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.

submitted to the EMBL Data Library, September 1995

A;Reference number: S63452

A;Accession: S63463

A;Molecule type: DNA

A;Residues: 1-835 <WAN>

A;Cross-references: EMBL:U36624; NID:g1276642; PID:g1039458; GSPDB:GN00016; MIPS:YPL019c

C;Genetics:

A;Gene: MIPS:YPL019c

A;Map position: 16L

Query Match 29.7%; Score 50.5; DB 2; Length 835;

Best Local Similarity 43.5%; Pred. No. 28;

Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 7 DEVYSRIPQPLFFINSEYFQYP 28

||: |||||

Db 466 DDIDSINPNPLRLRAGEYSKFP 488

RESULT 12

A36887

endo-alpha-sialidase (EC 3.2.1.129), tail - phage K1F

N:Alternate names: endo-N-acylneuraminidase

C:Species: phage K1F

C:Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A36887

J:Petter, J.G.; Vinar, E.R.

J: Bacteriol. 175, 4354-4363, 1993

A:Title: Complete nucleotide sequence of the bacteriophage K1F tail gene encoding endo-N

A:Reference number: A36887; MUID:93322313

A:Accession: A36887

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-920 <PE>

A:Cross-references: GB:M63657; NID:9215082; PIDN:AAC37340.1; PID:g215083

A:Note: In the authors' translation residues 875-888 are shown after residue 903 and, co

C:Keywords: glycosidase; hydrolase; polysaccharide degradation; tail protein

Query Match

Best Local Similarity 29.7%; Score 50.5; DB 2; Length 920;

Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 9 VYSRIP-QPLFFINSEYFQ 26

Db 295 VYERIPGPLYASEEFVQ 313

RESULT 13

B82744

conserved hypothetical protein XF0929 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: B82744

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82744

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-583 <SIM>

A:Cross-references: GB:AE003932; GB:AE003849; NID:99105849; PIDN:AAF83739.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., V.E.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0929

Query Match

Best Local Similarity 29.1%; Score 49.5; DB 2; Length 583;

Matches 9; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 WMFP-LGDEVYSRIPQPLFFINSEYF 25

Db 1 WMFP-LGDEVYSRIPQPLFFINSEYF 25

Db 63 WLFPHRGNELYSKPPMLMWLQAAFY 88

RESULT 14

T42642

phosphoinositide 3-kinase (EC 2.7.1.1) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000

C:Accession: T42642

R:Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.

J. Biol. Chem. 271, 13892-13899, 1996

A:Title: Cpk is a novel class of diophylla ptdIns 3-kinase containing a C2 domain

A:Reference number: 217659; MUID:96278830

A:Accession: T42642

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1658 <MO>

A:Cross-references: EMBL:U52193; NID:91272421; PID:g1272422; PIDN:AAC52604.1

A:Experimental source: strain balb c

C:Genetics:

A:Gene: cpk

C:Superfamily: Hsc2 phosphatidylinositol 3-kinase; protein kinase C C2 region homo

C:Keywords: phosphotransferase

Query Match 29.1%; Score 49.5; DB 2; Length 1658;

Best Local Similarity 42.3%; Pred. No. 88;

Matches 11; Conservative 2; Mismatches 8; Indels 5; Gaps 1;

QY 3 FPLGDEVYSRIPQPLFFINSEYFQY 28

Db 179 FPSTESVLRUPG----QSPYFSYP 199

RESULT 15

S73452

protein trsb - Mycoplasma pneumoniae (strain ATCC 29342)

N:Alternate names: hypothetical protein B01_orf299V

C:Species: Mycoplasma pneumoniae

A:Variety: ATCC 29342

C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C:Accession: S73452

R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneu

A:Reference number: S73327; MUID:97105885

A:Accession: S73452

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-299 <HIM>

A:Cross-references: EMBL:AE000015; GB:U00089; NID:91673779; PIDN:AAB95774.1; PID:91673779

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Gene: trsb

A:Genetic code: SGC3

A:Start codon: GTG

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match

Best Local Similarity 28.8%; Score 49; DB 2; Length 299;

Matches 10; Conservative 5; Mismatches 6; Indels 8; Gaps 1;

QY 10 YSRIPQPLFFI-----NSEYFQY 30

Db 271 YTWLPQPLAFFLGGLMALRTRKYRYPKN 299

Search completed: March 9, 2002, 00:34:10

Job time: 321 sec

RP VARIANT PHE-279.
 RX MEDLINE=98430412; PubMed=9759612;
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
 RA Yoshimizu N., Fukushi K., Satoh K.;
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
 RT for hypertension";
 RL Thromb. Haemost. 80:372-375(1998).
 CC -|- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -|- TISSUE SPECIFICITY: PLASMA.
 CC -|- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
 CC PRESENT IN 2% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
 CC RESPONSES.
 CC -|- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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 CC
 CC EMBL: U20157; AAC50126.1; -;
 CC DR EMBL: U24577; AAB04170.1; -;
 CC DR MIM: 601690; -;
 CC DR InterPro: IPR000379; Est_lip_thioest_actsite.
 CC DR InterPro: IPR000734; Lipase.
 CC DR PROSITE: PS00120; LIPASE_SER; 1.
 CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 441 PLATELET-ACTIVATING FACTOR
 FT
 FT ACT_SITE 273 273 ACETYLHYDROLASE.
 FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
 FT ACT_SITE 351 351 CHARGE RELAY SYSTEM.
 FT ACT_SITE 423 423 CHARGE RELAY SYSTEM.
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .).
 FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
 FT PROTEIN).
 FT
 FT MUTAGEN 108 108 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 FT MUTAGEN 273 273 S->A: LOSS OF ACTIVITY.
 FT MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.
 FT MUTAGEN 286 286 D->N: DIMINISHED ACTIVITY.
 FT MUTAGEN 296 296 D->A: LOSS OF ACTIVITY.
 FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.
 FT MUTAGEN 304 304 D->A: NO CHANGE IN ACTIVITY.
 FT MUTAGEN 338 338 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 FT MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.
 FT MUTAGEN 379 379 V -> A (IN REF. 2).
 FT CONFLICT 379 379
 FT SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

Query Match 100.0%; Score 170; DB 1; Length 441;
 Best Local Similarity 100.0%; Pred. No. 7.3e-17;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 |||||
 Db 298 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 327

RESULT 2

PAFA_BOVIN
 ID PAFA_BOVIN STANDARD; PRT; 444 AA.
 AC Q28017;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (LPL-ASSOCIATED
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LPL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LPL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Plasma;
 RC MEDLINE=96029630; PubMed=7592717;
 RX Tjoelker L.W., Stafforini D.M., Prescott S.M., Gray P.W.;
 RA McIntyre T.M.;
 RA "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad";
 RT J. Biol. Chem. 270:25481-25487(1995).
 RL -|- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -|- TISSUE SPECIFICITY: PLASMA.
 CC -|- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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 CC
 CC EMBL: U34247; AAC48483.1; -;
 CC DR InterPro: IPR000379; Est_lip_thioest_actsite.
 CC DR InterPro: IPR000734; Lipase.
 CC DR PROSITE: PS00120; LIPASE_SER; 1.
 CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 444 PLATELET-ACTIVATING FACTOR
 FT
 FT ACT_SITE 274 274 ACETYLHYDROLASE.
 FT ACT_SITE 297 297 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;

Query Match 91.2%; Score 155; DB 1; Length 444;
 Best Local Similarity 90.0%; Pred. No. 1e-14;
 Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 30
 |||||
 Db 299 WMFPLGDEVYSRIPOPLFFINSEYFOYPAN 328

RESULT 3

PAF_A_CANFA STANDARD: PRT: 444 AA.
 ID Q28262;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (EC 3.1.1.47)
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Statforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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 DR EMBL: U34246; AAC48484.1; -
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR InterPro: IPR000734; Lipase.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 DR Hydrolyase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 444
 FT BY SIMILARITY.
 FT PLATELET-ACTIVATING FACTOR
 FT ACETYLHYDROLASE.
 FT ACT_SITE 274 274
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 297 297
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 352 352
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 60 60
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 424 424
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 444 AA; 50136 MW; 814EFAE3B8074AC CRC64;

 Query Match 77.6%; Score 132; DB 1; Length 444;
 Best Local Similarity 76.7%; Pred. No. 1,9e-11;
 Matches 23; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

 QY 1 WMFPLGDEVYSRIPQPLFFINSEYFOYFAN 30
 |||||:|||||:|||||:|||||:|||||:|
 Db 299 WMLPLDDAIYSRIPQPLFFINSEYFOYFAN 328

 RESULT 4
 PAF_A_CAVPO STANDARD: PRT: 436 AA.
 ID

P70683;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (EC 3.1.1.47)
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7 OR PAFAH.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY; TISSUE=Liver;
 RX MEDLINE=97103479; PubMed=8947850;
 RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
 RA Yokoyama K., Setaka M., Nojima S.;
 RT "Cloning, expression and characterization of plasma
 RT platelet-activating factor-acetylhydrolase from guinea pig.";
 RL J. Biochem. 120:838-844(1996).
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC -----
 DR EMBL: D67037; BAAL1054.1; -
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR InterPro: IPR000734; Lipase.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 DR Hydrolyase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 436
 FT BY SIMILARITY.
 FT PLATELET-ACTIVATING FACTOR
 FT ACETYLHYDROLASE.
 FT ACT_SITE 271 271
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 294 294
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 349 349
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 76 76
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 324 324
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 436 AA; 49062 MW; C359D96E392FEE11 CRC64;

 Query Match 75.3%; Score 128; DB 1; Length 436;
 Best Local Similarity 80.8%; Pred. No. 7.1e-11;
 Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

 QY 1 WMFPLGDEVYSRIPQPLFFINSEYFQ 26
 |||||:|||||:|||||:|||||:|||||:|
 Db 296 WMFPVGEDVHSKIPQPLFFINSEYFQ 321

 RESULT 5
 PAF_A_CHICK STANDARD: PRT: 422 AA.
 ID
 AC Q90678;
 DT 01-NOV-1997 (Rel. 35, Created)

(EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).

DE PAFH2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase.";
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
RC TISSUE=Prostate;
RX MEDLINE=98161812; PubMed=9494101;
RA Rice S.O.J., Southan C., Boyd H.F., Terrett J.A., Macphie C.H.,
RA Moores K., Gloger I.S., Tew D.G.;
RT "Expression, purification and characterization of a human
RT serine-dependent phospholipase A2 with high specificity for oxidized
RT phospholipids and platelet activating factor.";
RL Biochem. J. 330:1309-1315(1998).
RN [3]
RP REVIEW.
RX MEDLINE=97364701; PubMed=9218411;
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RT "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -1- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLOURIDE,
CC 3,4-DICHLOROISOCOUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DFP) AND
CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT
CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO
CC AMYGDALA AND FRONTAL CORTEX.
CC -1- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.
CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.

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EMBL; D87845; BAA13468.1; -
DR ENBL; U89386; AAC39707.1; -
DR MM; 602344; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation.
FT ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 212 212 L -> F (IN REF. 2).
SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;

Query Match 45.9%; Score 78; DB 1; Length 392;
Best Local Similarity 53.8%; Pred. No. 0.00085;
Matches 14; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 WNFPLGDEVYSRIPQPLFFINSEYFQ 26
||||| : | : | : ||||| : |||
Db 261 WNFPLERDFYPKARGPVPFFINTEKFQ 286

RESULT 8
PAF2_BOVIN STANDARD; PRT; 392 AA.
ID AC P79106;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).
GN PAFH2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase.";
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RP REVIEW.
RX MEDLINE=97364701; PubMed=9218411;
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RT "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT
CC LOWER LEVELS IN OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.

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EMBL; D87559; BAA13419.1; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation.
FT ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 392 AA; 43865 MW; 1DEACA2ADF4CEA8 CRC64;

Query Match 45.3%; Score 77; DB 1; Length 392;
Best Local Similarity 53.8%; Pred. No. 0.0012;
Matches 14; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 WNFPLGDEVYSRIPQPLFFINSEYFQ 26
||||| : | : | : ||||| : |||

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Db 261 WMFPLEHDEYPTARGPIFFINAEKFQ 286
RESULT 9
PAPA_CAEEL STANDARD; PRT; 476 AA.
AC Q22943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLYHDROLASE HOMOLOG (EC 3.1.1.47).
GN C52B9.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Nelson J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SIMILARITY: STRONG, WITH VERTEBRATES PLATELET-ACTIVATING FACTOR
CC ACETYLYHDROLASE.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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CC -----
CC EMBL; U64598; AAK39216.1; -.
CC Wormpep; C5289.7; C606966.
CC InterPro; IPR000379; Est_lip_thioest_actsite.
CC InterPro; IPR000734; Lipase.
CC PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
KW Hypothetical protein; Hydrolase; Lipid degradation.
FT ACT_SITE 326 326 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 404 404 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 476 AA; 53974 MW; D61DF01F396371E9 CRC64;

Query Match 31.2%; Score 53; DB 1; Length 476;
Best Local Similarity 33.3%; Pred. No. 3.8;
Matches 10; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 1 WMFPLGDEVYSRIPQPLFFINSEYFOYPAN 30
||||| : ||| | : |
Db 351 WMYPLDSTQQEQAKOPTLFLNVDGQWNNEN 380

RESULT 10
M20_HUMAN STANDARD; PRT; 483 AA.
AC O60882;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MATRIX METALLOPROTEINASE-20 PRECURSOR (EC 3.4.24.-) (MMP-20) (ENAMEL
DE METALLOPROTEINASE) (ENAMELYSIN).
GN MMP20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.

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RC TISSUE-Odontoblast;
RX MEDLINE=98060762; PubMed=9398237;
RA Llano E., Pendas A.M., Knaeuper V., Sorsa T., Salo T., Salido E.,
RA Murphy G., Simmer J.P., Bartlett J.D., Lopez-Otin C.;
RT "Identification and structural and functional characterization of
RT human enamelysin (MMP-20).";
RL Biochemistry 36:15101-15108(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=20382723; PubMed=10922468;
RA Stracke J.O., Fosang A.J., Last K., Mercuri F.A., Pendas A.M.,
RA Llano E., Ferris R., Di Cesare P.E., Murphy G., Knaeuper V.;
RT "Matrix metalloproteinases 19 and 20 cleave aggrecan and cartilage
RT oligomeric matrix protein (COMP).";
RL FEBS Lett. 478:52-56(2000).
CC -!- FUNCTION: DEGRADATES AMELOGENIN, THE MAJOR PROTEIN COMPONENT OF THE
CC ENAMEL MATRIX AND TWO OF THE MACROMOLECULES CHARACTERISING THE
CC CARTILAGE EXTRACELLULAR MATRIX: AGGREGAN AND THE CARTILAGE
CC OLIGOMERIC MATRIX PROTEIN (COMP). MAY PLAY A CENTRAL ROLE IN TOOTH
CC ENAMEL FORMATION.
CC -!- CATALYTIC ACTIVITY: CLEAVES AGGREGAN AT THE 360-ASN-|-PHE-361
CC SITE.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
CC MATRIX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE ENAMEL ORGAN.
CC -!- PTM: AUTOACTIVATES AT LEAST AT THE 107-ASN-|-TYR-108 SITE (BY
CC SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A (ZINC
CC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
CC -----
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CC -----
CC EMBL; Y12779; CAA73317.1; -.
CC HSSP; P08254; IUSN.
CC MEROPS; M10.019; -.
CC MIM; 604629; -.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Matrixin.
CC InterPro; IPR000130; Zn_MTPeptdse.
CC Pfam; PF00045; hemopexin; 4.
CC PRINTS; PF00413; Peptidase_M10; 1.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC KW Hydrolase; Metalloprotease; Zinc; Calcium; Zymogen; Signal;
KW Extracellular matrix.
FT SIGNAL 1 22 POTENTIAL
FT PROPEP 23 107 BY SIMILARITY.
FT CHAIN 108 483 MATRIX METALLOPROTEINASE-20.
FT DOMAIN 293 483 HEMOPEXIN-LIKE.
FT SITE 100 100 CYSTEINE SWITCH (POTENTIAL).
FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 227 227 BY SIMILARITY.
FT METAL 230 230 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 296 483 POTENTIAL.
SQ SEQUENCE 483 AA; 54413 MW; 1DABBA04967AB395 CRC64;

Query Match 30.9%; Score 52.5; DB 1; Length 483;
Best Local Similarity 55.0%; Pred. No. 4.6;
Matches 11; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

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QY 9 VYSRIQ-PLFFINSEYFOY 27
  |||||
Db 398 VYLREPKTLFFVGDEYSY 417

RESULT 11
ALK1_YEAST
ID ALK1_YEAST STANDARD; PRT; 760 AA.
AC P43633;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE DNA DAMAGE-RESPONSIVE PROTEIN ALK1.
GN ALK1 OR YGI021W OR G3686.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rognes T.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Dellus H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YBL009W.
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DR EMBL; X87672; CAA61012.1; -
DR EMBL; Z72343; CAA96721.1; -
DR SGD; S0002989; ALK1.
KW DNA damage.
FT DOMAIN 240 245 POLY-GLN.
FT DOMAIN 264 269 POLY-SER.
FT DOMAIN 351 356 POLY-SER.
FT CONFLICT 758 760 LYK -> AL (IN REF. 1).
SQ SEQUENCE 760 AA; 86086 MW; 3FD169AD789ED60A CRC64;

Query Match 30.6%; Score 52; DB 1; Length 760;
Best Local Similarity 45.0%; Pred. No. 8.6;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 PLGDEVYSRIQPOPLFFINSE 23
  |||||
Db 636 PQDDVLYLRDLHPFLFLNGK 655

RESULT 12
NU2M_RHISA
ID NU2M_RHISA STANDARD; PRT; 313 AA.
AC O99817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
GN ND2.
OS Rhipicephalus sanguineus (Brown dog tick).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=34632;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=99083443; PubMed=9866211;
RA Black W.C. IV, Roehrdanz R.L.;
RT "Mitochondrial gene order is not conserved in arthropods: prostriate
RT and metastriate tick mitochondrial genomes.*";
RL Mol. Biol. Evol. 15:1772-1785(1998).
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
-----
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DR EMBL; AF081829; AAD05517.1; -
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1.1.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
KW SEQUENCE 313 AA; 37099 MW; E6382AEDAF32B0B6 CRC64;

Query Match 30.0%; Score 51; DB 1; Length 313;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 YSRIPQPLFFINSEY 24
  |||||
Db 270 YLRILTPLFFINSKP 284

RESULT 13
LOX1_HORVU
ID LOX1_HORVU STANDARD; PRT; 862 AA.
AC P29114; Q42845;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LIPOXYGENASE 1 (EC 1.13.11.12).
GN LOX1.1 OR LOXA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. TRIUMPH.
RX MEDLINE=95127754; PubMed=7827128;
RA van Mechelen J.R., Smits M., Douma A.C., Roustier J., Cameron-Mills V.,
RA Heidekamp F., Valk B.E.;
RT "Primary structure of a lipoxygenase from barley grain as deduced
RT from its cDNA sequence.*";
RL Biochim. Biophys. Acta 1254:221-225(1995).
RN [2]
RP SEQUENCE OF 274-294 AND 832-845.
RC STRAIN=CV. TRIUMPH; TISSUE=Embryo;
RX MEDLINE=92207997; PubMed=1554746;
RA Doderer A., Kockellink I., van der Veen S., Valk B.E., Schram A.W.,
RA Douma A.C.;
RT "Purification and characterization of two lipoxygenase isoenzymes
RT from germinating barley.*";
RL Biochim. Biophys. Acta 1120:97-104(1992).
CC -!- FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF
CC DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND
CC DEVELOPMENT, PEST RESISTANCE, AND SENESENCE OR RESPONSES TO
CC WOUNDING.
CC -!- CATALYTIC ACTIVITY: HYDROPEROXIDATION OF LIPIDS, CONTAINING A CIS,
CC CIS-1,4-PENTADIENE STRUCTURE.
CC -!- COFACTOR: IRON, ONE ATOM TIGHTLY BOUND PER MOLECULE.

```

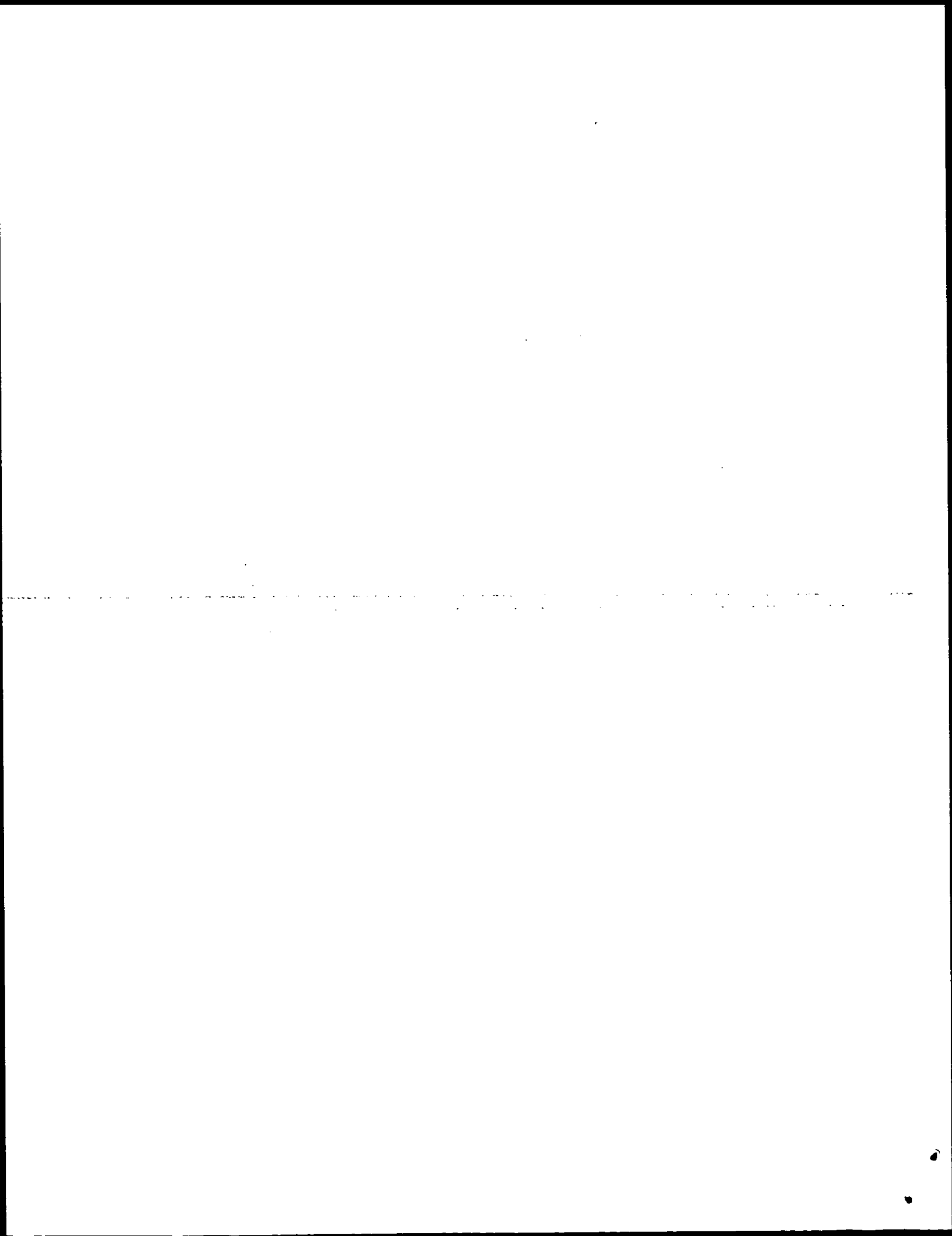

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF156956; AAF28472.1; JOINED.
DR EMBL; AF156947; AAF28472.1; JOINED.
DR EMBL; AF156948; AAF28472.1; JOINED.
DR EMBL; AF156949; AAF28472.1; JOINED.
DR EMBL; AF156950; AAF28472.1; JOINED.
DR EMBL; AF156951; AAF28472.1; JOINED.
DR EMBL; AF156952; AAF28472.1; JOINED.
DR EMBL; AF156953; AAF28472.1; JOINED.
DR EMBL; AF156954; AAF28472.1; JOINED.
DR EMBL; AF156955; AAF28472.1; JOINED.
DR EMBL; AF156956; AAF28472.1; JOINED.
DR MEROPS; M10.019; -.
DR MGD; MGI:1353466; Mmp20.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR003016; Lipoyl.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR000130; Zn_MTPeptidase.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; peptidase_M10; 1.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmG; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
KW Hydrolase; Metalloprotease; zinc; Calcium; zymogen; Signal;
KW Extracellular matrix.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 106 BY SIMILARITY.
FT CHAIN 107 482 MATRIX METALLOPROTEINASE-20.
FT DOMAIN 292 482 HEMOPEXIN-LIKE.
FT SITE 99 99 CYSTEINE SWITCH (POTENTIAL).
FT METAL 225 225 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 226 226 BY SIMILARITY.
FT METAL 229 229 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 235 235 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 295 482 BY SIMILARITY.
SQ SEQUENCE 482 AA; 54373 MW; 366149FAF2BDC8BB CRC64;

Query Match 29.1%; Score 49.5; DB 1; Length 482;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

OY 9 VYSRIPO-PLFFINSEYFOY 27
|| : || ||| : |||
Db 397 VYLKEPKQLFFVGEYYSY 416

Search completed: March 9, 2002, 00:47:35
Job time: 796 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:48 ; Search time 94.88 Seconds
(without alignments)
46.250 Million cell updates/sec

Title: US-09-922-067-2

Perfect score: 170

Sequence: 1 WMPPLGDEVSRIPQPLFFINSEYFQYPAN 30

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_todent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	56.5	346	11 Q9DB74	Q9db74 mus musculus
2	57	33.5	384	5 Q4753	Q4753 caenorhabditis
3	56	32.9	1183	3 Q9HDY4	Q9hdY4 schizosaccharomyces
4	54	31.8	872	4 Q9P221	Q9p221 homo sapien
5	52	30.6	215	1 Q58800	Q58800 pyrococcus
6	52	30.6	1038	2 Q45780	Q45780 bacteroides
7	52	30.6	2785	4 Q75691	Q75691 homo sapien
8	51.5	30.3	1253	6 Q97566	Q97566 canis famill
9	51	30.0	182	10 P93190	P93190 hordeum vul
10	51	30.0	864	10 Q9AXG8	Q9axg8 zea mays (m
11	50.5	29.7	835	3 Q02725	Q02725 saccharomyc
12	50	29.4	246	11 Q9D8N6	Q9d8n6 mus musculus
13	50	29.4	274	11 Q35590	Q35590 myocastor c
14	50	29.4	654	5 Q9VFX6	Q9vfx6 drosophila
15	50	29.4	728	3 Q9HFN3	Q9hfn3 candida tro
16	49.5	29.1	583	2 Q9PEU9	Q9peu9 xylella fas
17	49.5	29.1	1509	11 Q61194	Q61194 mus musculus
18	49.5	29.1	1658	11 Q61182	Q61182 mus musculus
19	49	28.8	139	11 Q9CSG5	Q9csg5 mus musculus

20	49	28.8	399	10 Q41695	Q41695 phaseolus a
21	49	28.8	489	2 Q9RRK7	Q9rrk7 deinococcus
22	49	28.8	600	2 Q9CEK0	Q9cek0 lactococcus
23	49	28.8	735	10 Q9FX21	Q9fx21 arabidopsis
24	49	28.8	858	10 Q9Z005	Q9zu05 perseia amer
25	48.5	28.5	91	12 Q89366	Q89366 paramescium
26	48	28.2	216	2 Q9KXC0	Q9kxc0 escherichia
27	48	28.2	216	9 Q9XJK7	Q9xjk7 bacterioph
28	48	28.2	546	2 Q07713	Q07713 staphylococ
29	48	28.2	690	5 Q9XWC5	Q9xwc5 caenorhabdi
30	48	28.2	726	2 Q9X839	Q9x839 streptomyce
31	47.5	27.9	290	5 Q9NGH8	Q9ngb8 tripneustes
32	47.5	27.9	316	2 Q9ABX5	Q9abx5 caulobacter
33	47.5	27.9	324	13 Q93507	Q93507 brachydanio
34	47.5	27.9	1155	2 Q9K0W2	Q9k0w2 vibrio chol
35	47.5	27.9	1604	3 Q14148	Q14148 schizosacch
36	47	27.6	255	2 Q9R9L8	Q9r9l8 rhizobium m
37	47	27.6	323	5 Q9N7R6	Q9n7r6 leishmania
38	47	27.6	332	2 Q9EX11	Q9ex11 streptomyce
39	47	27.6	388	4 Q95728	Q95728 homo sapien
40	47	27.6	448	13 Q99293	Q99293 xenopus lae
41	47	27.6	503	2 Q91362	Q91362 pseudomonas
42	47	27.6	558	10 Q9MI75	Q9mi75 arabidopsis
43	47	27.6	662	1 Q9HI06	Q9hi06 halobacteri
44	47	27.6	706	1 Q52000	Q52000 halobacteri
45	47	27.6	734	6 Q9BEG8	Q9beg8 bos taurus

ALIGNMENTS

RESULT 1
Q9DB74 Q9DB74 PRELIMINARY: PRT: 346 AA.
AC Q9DB74;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE PHOSPHOLIPASE A2 GROUP VII (PLATELET-ACTIVATING FACTOR)
DE ACETYLHYDROLASE, PLASMA).
GN PLA2G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 405:685-690(2001).
DR EMBL; AK005158; BAB23849.1; -;
DR MGB; MGI:1351327; Pla2g7.
DR InterPro; IPR000379; Est_lip-thioest_actsite.
DR InterPro; IPR000734; Lipase.

DR PROSITE: PS00120; LIPASE_SRP; UNKNOWN_1.
SQ SEQUENCE 346 AA; 38967 MW; D68A2A128402E554 CRC64;

Query Match 56.5%; Score 96; DB 11; Length 346;
Best Local Similarity 60.7%; Pred. No. 1.1e-05;
Matches 17; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOY 28
Db 297 WMYPVNEELYSRTLPQLLFINSAKTQT 324

RESULT 2
O44753 ID O44753 PRELIMINARY; PRT; 384 AA.

AC O44753;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE W03G9.6 PROTEIN.
GN W03G9.6.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
RX MEDLINE-94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Favello A., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Shalton N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Therry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.*;
RL Nature 368:32-38(1994).

RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
RA Dante M., Keppler D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039716; AAB96738.1; -;
DR InterPro; IPR00379; Est_lip_thioest_actsite.
SQ SEQUENCE 384 AA; 42888 MW; FDC1F97C162657C CRC64;

Query Match 33.5%; Score 57; DB 5; Length 384;
Best Local Similarity 33.3%; Pred. No. 4.3;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOY 30
Db 259 WMYPLDQOQEQAKQPMFLNVDGQWQNN 288

RESULT 3
O9HDY4 ID O9HDY4 PRELIMINARY; PRT; 1183 AA.

AC Q9HDY4;
DT 01-NAR-2001 (TREMBLrel. 16, Created)
DT 01-NAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE ATP DEPENDENT RNA HELICASE.

GN SPABIA10.06C.

OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-972H-;

RA O'Neil S., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.

DR EMBL; AL512562; CAC21479.1; -;

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001650; Helicase_C.

DR Pfam; PF00271; helicase_C; 1.

DR SMART; SM00487; DEXDC; 1.

DR SMART; SM00490; HELICc; 1.

KW ATP-binding; Helicase.

SQ SEQUENCE 1183 AA; 133995 MW; BA8183F0B4CA8BAF CRC64;

Query Match 32.9%; Score 56; DB 3; Length 1183;
Best Local Similarity 42.3%; Pred. No. 20;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 2 MFPLGDEVYSRIPQPLFFINSEYFOY 27

Db 1066 LFPSGSEVQVDPDRTYNIDSEYVY 1091

RESULT 4

Q9P221 ID Q9P221 PRELIMINARY; PRT; 872 AA.

AC Q9P221;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE KIA1507 PROTEIN (FRAGMENT).

GN KIA1507.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-20277482; PubMed=10819331;

RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;

RT "Prediction of the coding sequences of unidentified human

genes.XVII. The complete sequences of 100 new cDNA clones from brain

which code for large proteins in vitro.";

RL DNA Res. 7:143-150(2000).

DR EMBL; AB040940; BAA96031.1; -;

DR InterPro; IPR000765; GTP1_OBG.

DR PRINTS; PR00326; GTP1_OBG.

FT NON_TER 1

SQ SEQUENCE 872 AA; 98502 MW; 64C3ECC9DD23894E CRC64;

Query Match 31.8%; Score 54; DB 4; Length 872;
Best Local Similarity 33.3%; Pred. No. 28;
Matches 11; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

OY 1 WMFPLGDEVYSRIPQPLFFINSEYFOY 27

Db 257 WFFPSGREDLDFPEPVAFLNLRGDISGHWLQF 289

RESULT 5

O58800 ID O58800 PRELIMINARY; PRT; 215 AA.

RESULT 7

DR	HSP: P02751; 1FNA.
DR	InterPro: IPR003962; FmIII_repeat.
DR	InterPro: IPR003981; FN_III.
DR	InterPro: IPR002035; VWFA.
DR	Pfam: PF00041; fn3; 9.
DR	Pfam: PF00092; vwa; 2.
DR	PRINTS: PR0014; FNTYPEIII.
DR	PRINTS: PR00453; VWFADOMAIN.
DR	SMART: SM00060; FN3; 9.
DR	SMART: SM00327; VWA; 2.
DR	PROSITE: PS50234; VWFA; 2.
DR	Collagen; Repeat.
DR	NON_TER 1253 1253
DR	SEQUENCE 1253 AA; 133695 MW; 7FF2B500E4B8CA89 CRC64;
DR	FASTA

Query Match 30.3%; Score 51.5; DB 6; Length 1253;
Best Local Similarity 42.9%; Pred. No. 93;

Matches 12; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

Qy 4 PLGDEV-----YSRIQPLPFINSEY 24
 ||| : ||| : ||| : ||| :
 Db 1085 PLGQAVQVGLLSYSHRPSPLPLNSSY 1112

RESULT 9

Q02725 PRELIMINARY; PRT; 182 AA.
 AC Q02725;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE LIPOXYGENASE ISOMZYME 1 (EC 1.13.11.12) (LIPOXIDASE) (CAROTENE
 DE OXIDASE) (FRAGMENT).
 GN LOXI:HVL.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rousier J., Leah R., Mundy J., Cameron-Mills V.;
 RL Plant J. 0:0-0(0).
 CC -1- CATALYTIC ACTIVITY: LINOLEATE + O(2) -> (9Z,11E)-(13S)-13-
 CC HYDROPEROXYCYCLODECAN-9,11-DIENONE.
 CC -1- COFACTOR: IRON.
 DR EMBL; U83904; AAB41791.1; -;
 DR HSSP; P09186; 1LNH.
 DR Mendel; 13747; Horvu; Lox1:13747.
 DR InterPro; IPR001024; LH2.
 DR Pfam; PF01477; PLAT; 1.
 DR SMART; SM00308; LH2; 1.
 KW Oxidoreductase.
 FT NON_TER 182
 SQ SEQUENCE 182 AA: 19777 MW; 06B9D88E2E6C6717 CRC64;

Query Match 30.0%; Score 51; DB 10; Length 182;

Best Local Similarity 38.7%; Pred. No. 14;
 Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

Qy 1 WMFPLGDEVYSRIQPLPFINSEY--QYPA 29
 ||| : ||| : ||| : ||| :
 Db 146 WIYPAANYKRYNR-----FFANDTYLPSQMPA 172

RESULT 10

Q02725 PRELIMINARY; PRT; 864 AA.
 AC Q02725;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE LIPOXYGENASE.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilson R.A., Gardner H.W., Keller N.P.;
 RT "Cultivar-dependent expression of a maize lipoxigenase responsive to
 RT seed-infecting fungi."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF329371; AAG61118.1; -;
 SQ SEQUENCE 864 AA; 96476 MW; 639156E1C6EE8D2B CRC64;

Query Match 30.0%; Score 51; DB 10; Length 864;

Best Local Similarity 38.7%; Pred. No. 73;
 Matches 12; Conservative 4; Mismatches 9; Indels 6; Gaps 2;

Qy 1 WMFPLGDEVYSRIQPLPFINSEY--QYPA 29
 ||| : ||| : ||| : ||| :
 Db 144 WYIPAGKYRYNR-----FFSNDTYLPSQMPA 170

RESULT 11

Q02725 PRELIMINARY; PRT; 835 AA.
 AC Q02725;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE LPB12P.
 GN VTC3 OR LPB12C OR YPL019C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85061207; PubMed=6095044;
 RA Yang E., Friedberg E.C.;
 RT "Molecular cloning and nucleotide sequence analysis of the
 RT Saccharomyces cerevisiae RAD1 gene."
 RL Mol. Cell. Biol. 4:2161-2169(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92357722; PubMed=1379722;
 RA Stepien P.P., Margossian S.P., Landsman D., Butow R.A.;
 RT "The yeast nuclear gene suv3 affecting mitochondrial post-
 RT transcriptional processes encodes a putative ATP-dependent RNA
 RT helicase."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6813-6817(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95081072; PubMed=7989303;
 RA Hiser L., Hasson M.E., Rine J.;
 RT "ERG10 from Saccharomyces cerevisiae encodes acetoacetyl-CoA
 RT thiolase."
 RL J. Biol. Chem. 269:31383-31389(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97313271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albertmann K., Allen E., Ansoorge W.,
 RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
 RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
 RA Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,
 RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
 RA Humann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,
 RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
 RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
 RA Lewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,
 RA Network U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
 RA Purcell D., Schafer M., Scharfe M., Scherens B., Schramm S.,
 RA Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,
 RA Vierendeels F., Viissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
 RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
 RA Hani J.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
 RL Nature 387:0-0(0).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Wang Y., Ahmed A., Bussey H., Fortin N., Friesen J.D., Hall J.,
 RA Storms R.K., Vo D.H., Winnett E.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Jia Y., Cherry J.M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U36624; AAB68168.1; -
 DR SGD; S0005940; VTC3.
 DR InterPro; IPR001917; AminoTransf_2.
 DR InterPro; IPR001064; Crystallin.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 SQ SEQUENCE 835 AA; 96553 MW; F09BB36A9D9B9C11 CRC64;

Query Match 29.7%; Score 50.5; DB 3; Length 835;
 Best Local Similarity 43.5%; Pred. No. 83;
 Matches 10; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 7 DEVSRIPOPLFTINS-EYQYP 28
 Db 466 DDIDSINPLRLRAGEYSKFP 488
 : : | | | | : : | | : |

RESULT 12
 Q9D8N6 ID Q9D8N6 PRELIMINARY; PRT; 246 AA.
 AC Q9D8N6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 1810054G18RIK.
 GN 1810054G18RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 408:685-690(2001).
 EL EMBL; AK007858; BAB25310.1; -
 DR MGD; MGI:1922910; 1810054G18RIK.
 SQ SEQUENCE 246 AA; 28378 MW; 6FD6104D9945A81D CRC64;

Query Match 29.4%; Score 50; DB 11; Length 246;
 Best Local Similarity 71.4%; Pred. No. 26;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 PLGDEVYSRIPOPL 17
 Db 171 PLGDCRSRIPSPL 184
 : : | | | | | | | | | |

RESULT 13
 Q35590 ID Q35590 PRELIMINARY; PRT; 274 AA.
 AC Q35590;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE LECITHIN:CHOLESTEROL ACYL TRANSFERASE (FRAGMENT).
 GN LCAT.
 OS Myocastor coypus (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
 OX Myocastor.
 OX NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robinson M., Catzeflis F.M., Briolay J., Mouchiroud D.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U72324; AAB60792.1; -
 DR EMBL; U72323; AAB60792.1; JOINED.
 DR InterPro; IPR000734; Lipase.
 DR InterPro; IPR003386; LACT.
 DR Pfam; PF02450; LACT; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Transferase. 1 1
 FT NON_TER 274 274
 FT NON_TER
 SQ SEQUENCE 274 AA; 31979 MW; 29F87D1C5FF5B352 CRC64;

Query Match 29.4%; Score 50; DB 11; Length 274;
 Best Local Similarity 44.4%; Pred. No. 29;
 Matches 12; Conservative 6; Mismatches 5; Indels 4; Gaps 2;

QY 1 WMFPLGDEVYSRIPOPLFFINSEYFQY 27
 Db 155 WMFPL-NOV--PEGHVFISSQDFNY 177
 : : | | | | : : | | : |

RESULT 14
 Q9VFX6 ID Q9VFX6 PRELIMINARY; PRT; 654 AA.
 AC Q9VFX6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG8449 PROTEIN.
 GN CG8449.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe W., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 BA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Search completed: March 9, 2002, 00:46:51
Job time: 827 sec

Query Match	29.48;	Score 50;	DB 5;	Length 654;
-------------	--------	-----------	-------	-------------

QY 3 FPLGDEVYSRIPQLPFFINSEYFQYPAN 30
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D6 383 YPNNUVDHLVLRHALEMLNPKOFEXPPN 410

RESULT	15
ID	Q9HFN3
PRELIMINARY;	PRT; 728 AA.
AC	Q9HFN3;
DT	01-MAR-2001 (Tremblrel. 16, Created)
DD	01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	HEAT-SHOCK RELATED PROTEIN HSRL.
GN	HSRL.
OS	Candida tropicalis (Yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC	Saccharomycetales; mitospozic Saccharomycetales; Candida.
OX	NCBI_TaxID=5482;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	Serrano R.;
RA	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
[2]	
RN	SEQUENCE FROM N.A.
RP	Alli R., Pascual-Ahuir A., Marquez J.A., Malik K.A.;
RA	"Identification of Cadida tropicalis HSRL, a gene of the heat-shock
RT	factor related family which confers salt tolerance in Saccharmyces
RT	cerevisiae.";
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AJ296093; CACI2663.1; -.
DR	InterPro; IPR000232; HSF_DNA_bind.
DR	InterPro; IPR002341; HSF_ET5.
DR	InterPro; IPR002965; P-rich_extensio.
DR	Pfam; PF00447; HSF_DNA_bind; 2.
DR	PRINTS; PR00056; HSFDOMAIN.
DR	PRINTS; PR01217; PRICHEXTENS.
DR	PRODOM; PD001788; HSF_DNA_bind; 1.
DR	SMART; SM00415; HSF; 1.
DR	PROSITE; PS00434; HSF_DOMAIN; 1.
SO	SEQUENCE 728 AA; 80664 MW; 13D53EB4AB3A8B7A CRC64;

Query Match
29.48; Score 50; DB 3; Length 728;

us-09-922-067-2.rspt

Mon Mar 11 10:02:05 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 Seconds
(without alignments)
12.292 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101

Sequence: 1 WLMGNILRLFGSMTTPAN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID22/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	440	22	AAE00782 Mouse-Human plasma
2	101	100.0	440	22	AAE00783 Mouse-Human plasma
3	101	100.0	441	16	AAE00784 Human acetyl hydro
4	101	100.0	441	16	AAE00785 Human acetyl hydro
5	101	100.0	441	16	AAE00786 Human acetyl hydro
6	101	100.0	441	16	AAE00787 Human acetyl hydro
7	101	100.0	441	16	AAE00788 Human acetyl hydro
8	101	100.0	441	16	AAE00789 Human acetyl hydro
9	101	100.0	441	16	AAE00790 Human acetyl hydro
10	101	100.0	441	16	AAE00791 Human acetyl hydro
11	101	100.0	441	16	AAE00792 Human acetyl hydro

12	101	100.0	441	16	AAE00793 Human acetyl hydro
13	101	100.0	441	16	AAE00794 Human acetyl hydro
14	101	100.0	441	16	AAE00795 Human plasma plate
15	101	100.0	441	18	AAE00796 Human platelet-act
16	101	100.0	441	18	AAE00797 Human plasma plate
17	101	100.0	441	18	AAE00798 Platelet-activatin
18	101	100.0	441	19	AAE00799 Human plasma plate
19	101	100.0	441	20	AAE00800 Human PAF-AH prote
20	101	100.0	441	20	AAE00801 Plasma platelet-ac
21	101	100.0	441	21	AAE00802 Human low density
22	101	100.0	441	21	AAE00803 Human platelet-act
23	101	100.0	441	21	AAE00804 Human PAF-AH prote
24	101	100.0	441	21	AAE00805 Human plasma plate
25	101	100.0	441	22	AAE00806 Human plasma plate
26	101	100.0	441	22	AAE00807 Human plasma plate
27	101	100.0	441	22	AAE00808 Human platelet-act
28	101	100.0	441	22	AAE00809 Human plasma plate
29	101	100.0	441	22	AAE00810 Human plasma plate
30	101	100.0	441	22	AAE00811 Human plasma plate
31	101	100.0	441	22	AAE00812 Human plasma plate
32	101	100.0	441	22	AAE00813 Human plasma plate
33	101	100.0	441	22	AAE00814 Human platelet-act
34	101	100.0	441	22	AAE00815 Human plasma plate
35	101	100.0	441	22	AAE00816 Human platelet-act
36	101	100.0	441	22	AAE00817 Human plasma plate
37	101	100.0	441	22	AAE00818 Human plasma plate
38	101	100.0	441	22	AAE00819 Human plasma plate
39	101	100.0	441	22	AAE00820 Platelet-activatin
40	101	100.0	441	22	AAE00821 Human T-cell lymph
41	101	100.0	442	16	AAE00822 Macaque platelet-a
42	91	90.1	193	16	AAE00823 Macaque platelet-a
43	91	90.1	193	18	AAE00824 Macaque partial pl
44	91	90.1	193	18	AAE00825 Partial macaque pl
45	91	90.1	193	18	AAE00826

ALIGNMENTS

RESULT 1

AAE00782
ID AAE00782 standard; Protein; 440 AA.

XX AC AAE00782;

XX DT 02-JUL-2001 (first entry)

XX DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC1.

XX KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis; antiinflammatory; septicemia; inflammation; haemostasis; parturition;

XX KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX OS Chimeric - Mus sp.

XX OS Chimeric - Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 1..97
FT /note= "Corresponds to N-terminal 97 amino acids of mouse plasma platelet-activating factor acetylhydrolase (PAF-AH)"

FT Region 98..440

FT /note= "Corresponds to C-terminal 343 amino acids of human plasma platelet-activating factor acetylhydrolase (PAF-AH)"

US6203790-B1.

20-MAR-2001.

23-MAY-2000; 2000US-0577758.

07-JUN-1995; 95US-0480658.

PR 22-JAN-1998; 98US-0010715.
 PR 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0138905.
 XX (ICOS-) ICOS CORP.
 XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX WPI: 2001-280610/29.
 DR N-PSDB; AAD04168.
 XX
 XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF
 XX
 XX Example 8; Column -: 54pp; English.
 PS
 XX The present sequence is mouse-human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHC1.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 XX Sequence 440 AA;
 SQ
 Query Match 100.0%; Score 101; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WLMGNILRLFGSMTPAN 19
 Db 114 wlmgnilrlfsgmttpan 132
 RESULT 2
 AAEE00783
 ID AAE00783 standard; Protein; 440 AA.
 XX
 XX AAE00783;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 XX Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.
 XX
 XX Human: platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 1..40
 FT /note= "Corresponds to N-terminal 40 amino acids of mouse
 FT plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 FT Region 41..440
 FT /note= "Corresponds to C-terminal 400 amino acids of

FT human plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 XX
 PN US6203790-B1.
 XX
 PD 20-MAR-2001.
 XX
 PF 23-MAY-2000; 2000US-0577758.
 XX
 XX 07-JUN-1995; 95US-0480658.
 PR 22-JAN-1998; 98US-0010715.
 PR 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0318905.
 XX (ICOS-) ICOS CORP.
 XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX WPI: 2001-280610/29.
 DR N-PSDB; AAD04169.
 XX
 XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF
 XX
 XX Example 8; Column -: 54pp; English.
 PS
 XX The present sequence is mouse-human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHC2.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 XX Sequence 440 AA;
 SQ
 Query Match 100.0%; Score 101; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 WLMGNILRLFGSMTPAN 19
 Db 114 wlmgnilrlfsgmttpan 132
 RESULT 3
 AAAR73048
 ID AAR73048 standard; Protein; 441 AA.
 XX
 XX AAR73048;
 AC
 XX 06-DEC-1995 (first entry)
 DT
 XX Human acetyl hydrolase (AH) mutant C291S.
 DE
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 KW
 XX Homo sapiens.
 OS


```
XX Key Location/Qualifiers
FH Misc-difference 291
FT /note= "Wild-type Cys is substd. by Ser."
TT
XX
XX WO9509921-A.
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
PT
XX Example 10; : 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
DB 115 wlmgnilrlfsgmttpan 133

RESULT 4
AAR73049
ID AAR73049 standard; Protein; 441 AA.
XX
XX AAR73049;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C334S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 334
FT /note= "Wild-type Cys is substd. by Ser."
TT
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
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XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor,
PT acetylhydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
PT
XX Example 10; : 88pp; English.
XX
XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
DB 115 wlmgnilrlfsgmttpan 133

RESULT 5
AAR73050
ID AAR73050 standard; Protein; 441 AA.
XX
XX AAR73050;
XX
XX 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C407S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 407
FT /note= "Wild-type Cys is substd. by Ser."
TT
XX
XX WO9509921-A.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US11340.
XX
XX 06-OCT-1993; 93US-0133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
```

PT New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 PS Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

SQ Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSMTPAN 19
 |||||
 DB 115 wlmgnilrlflfgsmttpan 133

RESULT 6

ID AAR71920 standard; Protein; 441 AA.

AC AAR71920;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant S108A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given

CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSMTPAN 19
 |||||
 DB 115 wlmgnilrlflfgsmttpan 133

RESULT 7

ID AAR71921 standard; Protein; 441 AA.

AC AAR71921;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant S273A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
| | | | | | | | | | | | | | | | | | | | | |
Db 115 wlmgnilrlifgsmttpan 133

RESULT 8

AAR71922
ID AAR71922 standard; Protein; 441 AA.

XX AAR71922;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant D296A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 296
/note= "Wild-type Asp is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
| | | | | | | | | | | | | | | | | | | | | |
Db 115 wlmgnilrlifgsmttpan 133

RESULT 9

AAR71924
ID AAR71924 standard; Protein; 441 AA.

XX AAR71924;

XX 06-DEC-1995 (first entry)

AAR71923
ID AAR71923 standard; Protein; 441 AA.

XX AAR71923;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant D338A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 338
/note= "Wild-type Asp is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
| | | | | | | | | | | | | | | | | | | | | |
Db 115 wlmgnilrlifgsmttpan 133

RESULT 10

AAR71924
ID AAR71924 standard; Protein; 441 AA.

XX AAR71924;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant H351A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 351

FT /note= "Wild-type His is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

PT acetyl:hydrolase - useful in diagnosis and for treating

PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were made with single amino acid changes for the purposes of identifying the active site of AH. The sequences of these mutants are not given in the patent specification; they have been derived from the original wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory diseases, in particular pleurisy, asthma, rhinitis and eczema. The gene may also be used in raising monoclonal antibodies specific for AH that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTPAN 19

|||||

DB 115 wlmgnilrlifgsmttpan 133

RESULT 11

AAR71925

ID AAR71925 standard; Protein; 441 AA.

XX AAR71925;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant H395A/H399A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 395

FT /note= "Wild-type His is substd. by Ala."

FT 399

FT /note= "Wild-type His is substd. by Ala."

XX

PN WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

PT acetyl:hydrolase - useful in diagnosis and for treating

PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were made with single amino acid changes for the purposes of identifying the active site of AH. The sequences of these mutants are not given in the patent specification; they have been derived from the original wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory diseases, in particular pleurisy, asthma, rhinitis and eczema. The gene may also be used in raising monoclonal antibodies specific for AH that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 101; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTPAN 19

|||||

DB 115 wlmgnilrlifgsmttpan 133

RESULT 12

AAR73046

ID AAR73046 standard; Protein; 441 AA.

XX AAR73046;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C67S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 67

FT /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX

PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX Example 10; ; 88pp; English.
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 101; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
 Db 115 wlmgnilrlfsgmttpan 133
 |||||

RESULT 13
 AAR73047
 ID AAR73047 standard; Protein; 441 AA.
 XX AC AAR73047;
 XX 06-DEC-1995 (first entry)
 XX Human acetyl hydrolase (AH) mutant C229S.
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 229 /note= "Wild-type Cys is substd. by Ser."
 FT W09509921-A.
 XX 13-APR-1995.
 XX 06-OCT-1994; 94WO-US11340.
 XX 06-OCT-1993; 93US-0133803.
 XX (ICOS-) ICOS CORP.
 XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 101; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
 Db 115 wlmgnilrlfsgmttpan 133
 |||||

RESULT 14
 AAR71913
 ID AAR71913 standard; Protein; 441 AA.
 XX AC AAR71913;
 XX 05-DEC-1995 (first entry)
 XX Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX Homo sapiens.
 XX W09509921-A.
 XX 13-APR-1995.
 XX 06-OCT-1994; 94WO-US11340.
 XX 06-OCT-1993; 93US-0133803.
 XX (ICOS-) ICOS CORP.
 XX Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX N-PSDB; AAQ87947.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX Claim 5; Page 53-54; 88pp; English.
 XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
 CC is useful in the treatment of inflammatory diseases, in particular
 CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
 CC raising monoclonal antibodies specific for PAF-AH that are useful in
 CC the diagnosis of such diseases.
 XX Sequence 441 AA;
 SQ

Query Match 100.0%; Score 101; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: March 9, 2002, 00:31:57
Job time: 443 sec

OY 1 WLMGNILRLFGSMTTPAN 19
Db 115 wlmgnilrlfsgmttpan 133

RESULT 15

AAW26498
ID AAW26498 standard; Protein; 441 AA.

AC AAW26498;

DT 05-JAN-1998 (first entry)

Human platelet-activating factor acetylhydrolase.

Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation; asthma; pleurisy; necrotising enterocolitis; adult respiratory distress syndrome; therapy.

OS Homo sapiens.

PN US5656431-A.

PD 12-AUG-1997.

PF 06-OCT-1993; 93US-0133803.

PR 07-JUN-1995; 95US-0483232.

PR 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX Wilder CL;

XX WPI; 1997-414580/38.

XX N-PSDB; AAT87048.

XX Detecting lesions in human platelet-activating factor
XX acetylhydrolase gene - by comparison with defined wild-type gene
XX sequence

XX Example 3; Column 47-50; 53pp; English.

XX This polypeptide comprises human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH), a protein that inactivates PAF and
XX inactivates oxidatively fragmented phospholipids such as products of
XX the arachidonic acid cascade that mediate inflammation. Its
XX sequence was deduced from a full-length cDNA clone (see AAT87048)
XX obtained from a macrophage cDNA library. Mouse, dog, cattle,
XX chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have
XX also been identified. Recombinant PAF-AH polypeptides can be
XX produced in prokaryotic or eukaryotic host cells and used to mimic
XX or augment normal processes of resolution of inflammation in vivo.
XX Examples describe the in vivo therapeutic effect of recombinant
XX PAF-AH products on acute inflammation, pleurisy, asthma,
XX necrotising enterocolitis and adult respiratory distress syndrome
XX in animal models.

SQ Sequence 441 AA;

Query Match 100.0%; Score 101; DB 18; Length 441;

Best Local Similarity 100.0%; Pred. No. 6.2e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTTPAN 19
Db 115 wlmgnilrlfsgmttpan 133

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:32:59 ; Search time 47.03 Seconds
(without alignments)
9.091 Million cell updates/sec

Title: US-09-922-067-4
Perfect score: 101
Sequence: 1 WLMGNILRLFGSMTPAN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	19	2	US-08-557-892-4
2	101	100.0	19	2	US-08-387-858A-4
3	101	100.0	19	4	US-09-294-384B-4
4	101	100.0	441	1	US-08-470-187-8
5	101	100.0	441	1	US-08-318-905-8
6	101	100.0	441	1	US-08-483-232-8
7	101	100.0	441	1	US-08-483-140-8
8	101	100.0	441	2	US-08-485-938A-8
9	101	100.0	441	3	US-09-328-474-8
10	101	100.0	441	3	US-09-100-546-8
11	101	100.0	441	3	US-09-010-715-8
12	101	100.0	441	4	US-09-577-758-8
13	101	100.0	441	4	US-08-483-140-30
14	91	90.1	193	1	US-08-485-938A-36
15	91	90.1	193	2	US-08-483-140-28
16	77	76.2	444	1	US-08-485-938A-32
17	77	76.2	444	2	US-08-485-938A-33
18	72	71.3	444	2	US-08-483-140-27
19	68	67.3	440	1	US-08-485-938A-31
20	68	67.3	440	2	US-08-121-713D-58
21	44	43.6	730	1	US-08-835-266-58
22	44	43.6	730	2	US-09-060-692-58
23	44	43.6	730	2	US-08-893-391-58
24	44	43.6	730	3	PCT-US94-10151A-58
25	44	43.6	730	5	US-08-770-301A-1
26	42	41.6	999	2	US-09-175-581-1
27	42	41.6	999	3	US-09-175-581-1

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 62, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 12, Appli

28 42 41.6 1023 2 US-08-475-891A-2
29 42 41.6 1023 2 US-08-567-375-2
30 42 41.6 1023 2 US-08-587-680A-2
31 40 39.6 347 1 US-08-118-270-47
32 40 39.6 347 5 PCT-US93-08528-47
33 40 39.6 363 1 US-08-148-209A-2
34 40 39.6 363 1 US-08-148-209A-3
35 40 39.6 1382 3 US-09-057-570-4
36 40 39.6 1657 3 US-09-057-570-2
37 40 39.6 1805 3 US-09-057-570-7
38 39 38.6 313 3 US-08-926-842B-62
39 39 38.6 377 3 US-09-150-133-5
40 39 38.6 377 3 US-09-150-141-5
41 39 38.6 377 4 US-09-374-493-5
42 39 38.6 377 4 US-09-374-824-5
43 39 38.6 377 4 US-09-374-492-5
44 38 37.6 125 5 PCT-US93-06829-2
45 38 37.6 125 5 PCT-US93-06829-12

ALIGNMENTS

RESULT 1
US-08-557-892-4
: Sequence 4, Application US/08557892
: Patent No. 5968818
: GENERAL INFORMATION:
: APPLICANT: MacPhee, Colin Houston
: APPLICANT: Tew, David Graham
: APPLICANT: Southan, Christopher Donald
: APPLICANT: Hickey, Dierdre Mary Bernadette
: APPLICANT: Gloger, Israel Simon
: APPLICANT: Lawrence, Geoffrey Mark Prouse
: APPLICANT: Rice, Simon Quentyn John
: TITLE OF INVENTION: Compounds
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/557,892
: FILING DATE: 14 No. 5968818ember 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/387,858
: FILING DATE: 14 No. 5968818ember 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Dustman, Wayne J.
: REGISTRATION NUMBER: 33,870
: REFERENCE/DOCKET NUMBER: P30893C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5023
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 19 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FRAGMENT TYPE: internal
US-08-557-892-4

Query Match 100.0%; Score 101; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTTPAN 19
Db 1 WLMGNILRLFGSMTTPAN 19

RESULT 2

US-08-387-858A-4
; Sequence 4, Application US/08387858A
; Patent No. 5981252
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quantyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858A
; FILING DATE: 24 February 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-387-858A-4

Query Match 100.0%; Score 101; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTTPAN 19
Db 1 WLMGNILRLFGSMTTPAN 19

RESULT 3

US-08-470-187-8

US-09-294-384B-4
; Sequence 4, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quantyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,384B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-09-294-384B-4

Query Match 100.0%; Score 101; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTTPAN 19
Db 1 WLMGNILRLFGSMTTPAN 19

RESULT 4

US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl

;; TITLE OF INVENTION: Hydrolase
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470.187
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5532152and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31672
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-470-187-8

Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTPAN 19
|||||
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 5
US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/318,905
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5641669and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 32205
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-318-905-8

Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLMGNILRLFGSMTPAN 19
|||||
Db 115 WLMGNILRLFGSMTPAN 133

RESULT 6
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-8402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-232-8

Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
|||||
DB 115 WLMGNILRLFGSMTPAN 133

RESULT 7
US-08-483-140-8
; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-8

Query Match 100.0%; Score 101; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
|||||
DB 115 WLMGNILRLFGSMTPAN 133

RESULT 8
US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match 100.0%; Score 101; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
|||||
DB 115 WLMGNILRLFGSMTPAN 133

RESULT 9
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-041-8

Query Match 100.0%; Score 101; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
DB 115 WLMGNILRLFGSMTPAN 133

RESULT 10
US-09-328-474-8
Sequence 8, Application US/09328474
Patent No. 6045794
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,474
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-328-474-8

Query Match 100.0%; Score 101; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPAN 19
DB 115 WLMGNILRLFGSMTPAN 133

RESULT 11
US-09-100-546-8
Sequence 8, Application US/09100546
Patent No. 6099836
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

RESULT 13

US-09-577-758-8
; Sequence 8, Application US/09577758
; Patent No. 6203790

FILE NO. 0203790
: GENERAL INFORMATION:

APPLICANT: Cousins, Lawrence
APPLICANT: Eberhardt, Chris
APPLICANT: Gray, Patrick W.

RESULT 12
US-09-010-715-8

```

1  TITLE OF INVENTION: Acetylhydrolase
2  NUMBER OF SEQUENCES: 30
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
5  STREET: 6300 Sears Tower, 233 South Wacker Drive
6  CITY: Chicago
7  STATE: Illinois
8  COUNTRY: United States of America
9  ZIP: 60606-6402
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/577,758
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 09/010,715
21 FILING DATE:

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: FILING DATE:
 : PRIOR APPLICATION NUMBER: US 08/133,803
 : APPLICATION NUMBER: 06-OCT-1993
 : FILING DATE: 06-OCT-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: NO. 6203790and, Greta E.
 : REGISTRATION NUMBER: 35,302
 : REFERENCE/DOCKET NUMBER: 27866/32793
 : TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-577-758-8

Query Match 100.0%; Score 101; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTTPAN 19
Db 115 WLMGNILRLFGSMTTPAN 133
|||||

RESULT 14
US-08-483-140-30
Sequence 30, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
HYDROLASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.140
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-30

Query Match 90.1%; Score 91; DB 1; Length 193;
Best Local Similarity 89.5%; Pred. No. 1.4e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTTPAN 19
Db 73 WLMGNILRLFGSMTTPAN 91
|||||

RESULT 15
US-08-485-938A-36
Sequence 36, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
HYDROLASE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-36

Query Match 90.1%; Score 91; DB 2; Length 193;
Best Local Similarity 89.5%; Pred. No. 1.4e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTTPAN 19
Db 73 WLMGNILRLFGSMTTPAN 91
|||||

Search completed: March 9, 2002, 00:33:00
Job time: 401 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:10 ; Search time 53.53 Seconds
(without alignments)
27.037 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101
Sequence: 1 WLMGNILRLFLGSMTPAN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	441	2 S60247	platelet-activatin
2	48	47.5	436	2 JC5021	platelet-activatin
3	46	45.5	410	2 D83923	spore germination
4	45.5	45.0	247	2 S59523	triose-phosphate i
5	45	44.6	417	2 D82111	uracil permease VC
6	44	43.6	122	2 T16624	hypothetical prote
7	44	43.6	448	2 A26190	glucuronate permease
8	44	43.6	730	2 JH0798	fasciclin IV precu
9	43	42.6	185	2 H72259	ribosome recycling
10	43	42.6	422	2 S74561	hypothetical prote
11	43	42.6	836	2 D82177	conserved hypothet
12	42.5	42.1	403	2 D75333	conserved hypothet
13	42	41.6	422	2 G83503	probable MFS trans
14	42	41.6	476	2 H96802	probable amino aci
15	42	41.6	999	2 JC5278	oxygen-regulated p
16	41	40.6	266	2 F83741	hypothetical prote
17	41	40.6	308	1 H65050	probable Arp-bindi
18	41	40.6	308	2 C85919	hypothetical prote
19	41	40.6	338	2 S24930	hypothetical prote
20	41	40.6	444	2 G69905	glucuronate permease
21	41	40.6	448	2 JC2305	annexin - chicken
22	41	40.6	671	2 JC2029	hypothetical prote
23	41	40.6	1817	2 T34249	triose-phosphate i
24	40.5	40.1	247	2 S18604	hypothetical prote
25	40	39.6	123	2 H72698	hypothetical prote
26	40	39.6	204	2 S07786	hypothetical prote
27	40	39.6	233	2 T24714	hypothetical prote
28	40	39.6	251	2 T40671	flir protein - Cau
29	40	39.6	256	2 T24713	hypothetical prote

30 40 39.6 278 2 S64317 probable membrane
31 40 39.6 316 2 T00769 hypothetical prote
32 40 39.6 363 2 I48261 angiotensin II rec
33 40 39.6 363 2 A49092 angiotensin II rec
34 40 39.6 363 2 JC2543 angiotensin II rec
35 40 39.6 427 2 F83066 uracil permease PA
36 40 39.6 432 2 F71152 probable lipopolys
37 40 39.6 664 2 B53610 ntpr protein - Ent
38 40 39.6 1098 2 B70232 hypothetical prote
39 40 39.6 1107 2 T25450 hypothetical prote
40 39.6 1345 2 S46817 hypothetical prote
41 40 39.6 1778 2 T50074 probable nucleopor
42 40 39.6 1867 2 S22775 MOR1 protein - yea
43 39.5 39.1 146 2 F82048 conserved hypothet
44 39.5 39.1 240 2 B82833 conserved hypothet
45 39 38.6 165 2 F81734 conserved hypothet

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf,

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:G780132; PIDN:AAC50126.1; PID:G780133

Query Match 100.0%; Score 101; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WLMGNILRLFLGSMTPAN 19

Db 115 WLMGNILRLFLGSMTPAN 133

RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama,

J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KARL>

A:Cross-references: DDBJ:D67037; NID:G1644228; PIDN:BA11054.1; PID:G1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 133-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

C:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:23-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>

F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.5%; Score 48; DB 2; Length 436;
 Best Local Similarity 50.0%; Pred. No. 3;
 Matches 8; Conservative 5; Mismatches 0; Gaps 0;

QY 3 MGNILRLFLFGSMTPA 18
 :|:|:|:|:|:|
 Db 117 LGKLLKLLYGSVKVPA 132

RESULT 3
 D83923
 spore germination protein I gerAA [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 C:Accession: D83923
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20263314
 A:Accession: D83923
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-410 <STO>
 A:Cross-references: GB:AP001514; GB:BA000004; NID:gi0174613; PIDN:BA05907.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: gerAA

Query Match 45.5%; Score 46; DB 2; Length 410;
 Best Local Similarity 47.8%; Pred. No. 6.1;
 Matches 11; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 WLMGNILRL-----FGSMTP 17
 :|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 213 WLMGSAURLRLRITFFIGFVLTP 235

RESULT 4
 S59523
 triose-phosphate isomerase (EC 5.3.1.1) 1, cytosolic - red alga (Gracilaria verrucosa)
 C:Species: Gracilaria verrucosa
 C:Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 20-Apr-2000
 C:Accession: S59523; S59530
 R:Zhou, Y.H.; Ragan, M.A.
 Curr. Genet. 28, 317-323, 1995
 A:Title: Cloning and characterization of the nuclear gene and cDNAs for triosephosphate
 A:Reference number: S59530; MUID:96120860
 A:Accession: S59523
 A:Molecule type: mRNA
 A:Residues: 1-247 <ZHO>
 A:Cross-references: EMBL:L38662
 A:Accession: S59530
 A:Molecule type: DNA
 A:Residues: 5-247 <ZHW>
 A:Cross-references: EMBL:L38662
 C:Genetics:
 A:Gene: TP11
 C:Superfamily: triose-phosphate isomerase
 C:Keywords: cytosol; gluconeogenesis; glycolysis; homodimer; intramolecular oxidoreductase
 F:84,157/Active site: His, Glu #status predicted

Query Match 45.0%; Score 45.5; DB 2; Length 247;
 Best Local Similarity 34.8%; Pred. No. 4.3;
 Matches 9; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 1 WLMGNI-----LRLFLFGSMTPAN 19
 :|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 183 WLANNVSPQVAASRILYGGVGSVPAN 208

RESULT 5

D82111
 uracil permease VC2171 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio Cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: D82111
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson,
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Seller
 L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833
 A:Accession: D82111
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-417 <HEI>
 A:Cross-references: GB:AE004288; GB:AE003852; NID:9956710; PIDN:AAF95316.1; GSPDB:
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2171
 A:Map position: 1
 C:Superfamily: uracil transport protein uraA

Query Match 44.6%; Score 45; DB 2; Length 417;
 Best Local Similarity 60.0%; Pred. No. 9.1;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMGNILRLFLFGSMTP 16

:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 323 VMGGIMILLFGSIAT 337

RESULT 6

TI6624
 hypothetical protein M02D8.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: TI6624

R:Miller, N.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid M02D8.
 A:Reference number: Z18549
 A:Accession: TI6624
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-122 <MIL>
 A:Cross-references: EMBL:U41034; NID:gi086742; PID:gi086744; PIDN:AAA82380.1; CESP:
 C:Genetics:
 A:Gene: CESP:M02D8.2
 A:Introns: 77/2

Query Match 43.6%; Score 44; DB 2; Length 122;
 Best Local Similarity 44.4%; Pred. No. 3.7;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLFGSMTPA 18

:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 73 WVDGDIIRLVFNPSPTGA 90

RESULT 7

A26190
 gluconate permease gntP - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jul-2000
 C:Accession: A26190; D69636

R:Fujita, Y.; Fujita, T.; Miwa, Y.; Nihashi, J.; Aratani, Y.
 J. Biol. Chem. 261, 13744-13753, 1986
 A:Title: Organization and transcription of the gluconate operon, gnt, of Bacillus
 A:Reference number: A92561; MUID:87008613
 A:Accession: A26190

Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833
 A:Accession: D82177
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-836 <HEI>
 A:Cross-references: GB:AE004240; GB:AE003852; NID:g9656133; PIDN:AAF94780.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1629
 A:Map position: 1

Query Match 42.6%; Score 43; DB 2; Length 836;
 Best Local Similarity 38.9%; Pred. No. 41;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 WLMGNILRLFGSMTPPA 18
 I: ||| ||| :
 Db 319 WVCNVGLGLLANQLIPS 336
 I: ||| ||| : I:

RESULT 12
 D75333
 conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: D75333
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: D75333
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-403 <WHI>
 A:Cross-references: GB:AE002033; GB:AE000513; NID:g6459726; PIDN:AAF11493.1; PID:g645972
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1940
 A:Map position: 1

Query Match 42.1%; Score 42.5; DB 2; Length 403;
 Best Local Similarity 58.8%; Pred. No. 23; Mismatches 2; Indels 0; Gaps 1;
 Matches 10; Conservative 2; Indels 5; Gaps 1;
 QY 8 RLFP-----GSMTPPAN 19
 I: ||| ||||| I:
 Db 150 RLVFAPAAGGSMTPSN 166
 I: ||| ||||| I:

RESULT 13
 G83503
 probable MFS transporter PA1131 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: G83503
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: G83503
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <STO>
 A:Cross-references: GB:AE004543; GB:AE004091; NID:g9947047; PIDN:AAG04520.1; GSPDB:GN001
 A:Experimental source: strain PA01

C:Genetics:
 A:Gene: PA1131

Query Match 41.6%; Score 42; DB 2; Length 422;
 Best Local Similarity 44.4%; Pred. No. 30;
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTPPA 18
 I: ||| ||| :
 Db 320 WLVCALLPFLGSLATPA 337
 I: ||| ||| :

RESULT 14
 H96802
 probable amino acid carrier [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: H96802
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Dewar
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: H96802
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-476 <STO>
 A:Cross-references: GB:AE005173; NID:g11079491; PIDN:AAG29203.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F2P24.9
 A:Map position: 1
 C:Superfamily: *Arabidopsis* amino acid transport protein I

Query Match 41.6%; Score 42; DB 2; Length 476;
 Best Local Similarity 46.7%; Pred. No. 34;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WLMGNILRLFGSMTP 15
 I: ||| ||| : I:
 Db 62 WLGPVVMVLLFSVAVT 76
 I: ||| ||| : I:

RESULT 15
 JC5278
 oxygen-regulated protein 150K precursor - human
 C:Species: *Homo sapiens* (man)
 C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
 C:Accession: JC5278; PC4308
 R:Ikeda, J.; Kaneda, S.; Kuwabara, K.; Ogawa, S.; Kobayashi, T.; Matsumoto, M.; Yur
 Biochem. Biophys. Res. Commun. 230, 94-99, 1997
 A:Title: Cloning and expression of cDNA encoding the human 150 kDa oxygen-regulated
 A:Reference number: JC5278; MUID:97148579
 A:Accession: JC5278
 A:Molecule type: mRNA
 A:Residues: 1-999 <IKE1>
 A:Cross-references: GB:U65785; NID:g1794218; PIDN:AAC50947.1; PID:g1794219
 A:Accession: PC4308
 A:Molecule type: protein
 A:Residues: 33-63 <IKE2>
 A:Experimental source: astrocytoma U373
 C:Comment: This protein plays a role in protein folding and secretion in the endopl
 F;33-999/Product: oxygen-regulated protein 150K #status predicted <MAP>

Query Match 41.6%; Score 42; DB 2; Length 999;

Best Local Similarity 53.3%; Pred. No. 74;
Matches 8; Conservative 2; Mismatches

5; Indels 0; Gaps 0;

QY 3 MGNILRLFLFGSMTP 17

:|| : ||| |||

Db 577 LGNTISSLFGGGTTP 591

Search completed: March 9, 2002, 00:34:11
Job time: 322 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:35 ; Search time 30.16 Seconds
(without alignments)
23.098 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101

Sequence: 1 WLMGNILRLFGSMTPAN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	441	1 PAPA_HUMAN	Q13093 h platelet-
2	77	76.2	444	1 PAPA_CANFA	Q28262 c platelet-
3	72	71.3	444	1 PAPA_BOVIN	Q28017 b platelet-
4	68	67.3	440	1 PAPA_MOUSE	O60963 m platelet-
5	48	47.5	436	1 PAPA_CAVPO	P70583 c platelet-
6	45.5	45.0	250	1 TPTS_GRAVE	P48492 gracilaria
7	44	43.6	448	1 GNTF_BACSU	P12012 bacillus su
8	44	43.6	730	1 SMIA_SCHAM	Q26473 schistocerc
9	43	42.6	185	1 RRF_THEMA	O9x1b9 thermotoga
10	42	41.6	999	1 ORRP_HUMAN	O9y411 homo sapien
11	41	40.6	321	1 GUTO_ECOLI	P17115 escherichia
12	41	40.6	338	1 Y3BK_CORSE	Q39635 corydalis s
13	41	40.6	444	1 YOJA_BACSU	O31862 bacillus su
14	41	40.6	448	1 GNTF_BACLI	P46832 bacillus li
15	41	40.6	618	1 ANX6_BOVIN	P79134 bos taurus
16	41	40.6	671	1 ANX6_CHICK	P51901 gallus gall
17	40.5	40.1	247	1 TPTS_DROME	P29613 drosophila
18	40	39.6	37	1 YBGT_ECOLI	P56100 escherichia
19	40	39.6	204	1 YPOB_STYLE	P14289 stytonychia
20	40	39.6	251	1 FLIR_CAUCR	Q45975 caulobacter
21	40	39.6	278	1 YG1I_YEAST	P53217 saccharomyc
22	40	39.6	363	1 AG22_HUMAN	P50052 homo sapien
23	40	39.6	363	1 AG22_MERUN	O9z026 meriones un
24	40	39.6	363	1 AG22_MOUSE	P35374 mus musculus
25	40	39.6	363	1 AG22_RAT	P35351 rattus norv
26	40	39.6	664	1 NTP1_ENTHR	P43439 enterococcu
27	40	39.6	1345	1 YHO0_YEAST	P38800 saccharomyc
28	40	39.6	1867	1 MOT1_YEAST	P32333 saccharomyc
29	39	38.6	120	1 CHH1_PENNO	O97383 penaeus mon
30	39	38.6	377	1 TPTS_HUMAN	O60704 homo sapien
31	39	38.6	414	1 URAA_HAEIN	P45117 haemophilus
32	39	38.6	457	1 SYC_RICPR	Q9ze62 rickettsia
33	39	38.6	672	1 ANX6_HUMAN	P08133 homo sapien

34	39	38.6	672	1 ANX6_MOUSE	P14824 mus musculus
35	39	38.6	672	1 ANX6_RAT	P48037 rattus norv
36	39	38.6	824	1 YOT5_CAEEL	P34651 caenorhabdi
37	39	38.6	1011	1 PPOI_CHICK	P26446 gallus gall
38	38.5	38.1	253	1 TPTS_ORYSA	P48494 oryza sativ
39	38.5	38.1	444	1 YHDP_BACSU	O07585 bacillus su
40	38	37.6	249	1 CDSA_ECOLI	P06466 e phosphati
41	38	37.6	251	1 TPTS_VIBSA	Q56738 vibrio sp.
42	38	37.6	260	1 AG22_SHEEP	Q28929 ovis aries
43	38	37.6	313	1 YOO6_YEAST	Q12094 saccharomyc
44	38	37.6	320	1 MCA2_HUMAN	Q13155 homo sapien
45	38	37.6	341	1 SYFA_MYCPN	P75564 mycoplasma

ALIGNMENTS

RESULT	1				
ID	PAPA_HUMAN	STANDARD:	PRT:	441 AA.	
AC	Q13093: Q15692;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)				
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED				
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE				
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).				
GN	PLA2G7 OR PAFAH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.				
RC	TISSUE=Myeloid;				
RC	MEDLINE=95214779; PubMed=7700381;				
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,				
RA	Schlimp B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,				
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;				
RA	"Anti-inflammatory properties of a platelet-activating factor				
RT	acetylhydrolase.";				
RL	Nature 374:549-553(1995).				
[2]					
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
TISSUE=Lymphoma;					
MEDLINE=96197208; PubMed=8624782;					
RC	Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,				
RC	Moore K., Gloger I.S., Macphie C.H.;				
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-				
RT	associated, serine-dependent phospholipase involved in the oxidative				
RL	modification of low-density lipoproteins.";				
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).				
[3]					
MUTAGENESIS.					
MEDLINE=96029630; PubMed=7592717;					
RA	Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,				
RA	Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,				
RA	Gray P.W.;				
RT	"Plasma platelet-activating factor acetylhydrolase is a secreted				
RT	phospholipase A2 with a catalytic triad.";				
RL	J. Biol. Chem. 270:25481-25487(1995).				
[4]					
VARIANT PHE-279.					
MEDLINE=96259525; PubMed=8675689;					
RA	Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,				
RA	Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,				
RA	McIntyre T.M., Gray P.W., Prescott S.M.;				
RT	"Platelet-activating factor acetylhydrolase deficiency. A missense				
RT	mutation near the active site of an anti-inflammatory				
RT	phospholipase.";				
RL	J. Clin. Invest. 97:2784-2791(1996).				
[5]					

RP VARIANT PHE-279.
 RX MEDLINE=98430412; PubMed=9759612;
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
 RA Yoshimizu N., Fukushi K., Satch K.;
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
 RL thromb. Haemost. 80:372-375(1998).
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
 CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
 CC RESPONSES.
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U20157; AAC50126.1; -;
 CC EMBL: U24577; AAB041170.1; -;
 CC MIM: 601690;
 CC InterPro: IPR000379; Est_lip_thioest_actsite.
 CC InterPro: IPR000734; Lipase.
 CC PROSITE: PS00120; LIPASE_SER: 1.
 CC Hydrolase; Lipid degradation; Glycoprotein; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 441
 CC ACT_SITE 273 273 PLATELET-ACTIVATING FACTOR
 CC ACT_SITE 296 296 ACETYLHYDROLASE.
 CC ACT_SITE 351 351 CHARGE RELAY SYSTEM.
 CC CARBOHYD 423 423 CHARGE RELAY SYSTEM.
 CC CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
 CC PROTEIN).
 CC MUTAGEN 108 108 /FTIG-VAR_004268.
 CC MUTAGEN 273 273 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 CC MUTAGEN 286 286 S->A: LOSS OF ACTIVITY.
 CC MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.
 CC MUTAGEN 296 296 D->N: DIMINISHED ACTIVITY.
 CC MUTAGEN 296 296 D->A: LOSS OF ACTIVITY.
 CC MUTAGEN 304 304 D->N: LOSS OF ACTIVITY.
 CC MUTAGEN 338 338 D->A: NO CHANGE IN ACTIVITY.
 CC MUTAGEN 351 351 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 CC MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.
 CC CONFLICT 379 379 V -> A (IN REF. 2).
 CC SEQUENCE 441 AA; 50077 MW; 3BA9DEA9E8094A57 CRC64;

Query Match 100.0%; Score 101; DB 1; Length 441;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WLMGNILRLFGSMTPAN 19
 Db 115 WLMGNILRLFGSMTPAN 133

RESULT 2

PAFA_CANFA STANDARD; PRT; 444 AA.
 ID PAFA_CANFA
 AC Q28262;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE (EC 3.1.1.47)
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Plasma;
 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U34246; AAC48484.1; -;
 CC InterPro: IPR000379; Est_lip_thioest_actsite.
 CC InterPro: IPR000734; Lipase.
 CC PROSITE: PS00120; LIPASE_SER: 1.
 CC Hydrolase; Lipid degradation; Glycoprotein; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 444
 CC ACT_SITE 274 274 PLATELET-ACTIVATING FACTOR
 CC ACT_SITE 297 297 ACETYLHYDROLASE.
 CC ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC CARBOHYD 60 60 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 444 AA; 50136 MW; 814EF0AE38B074AC CRC64;
 Query Match 76.2%; Score 77; DB 1; Length 444;
 Best Local Similarity 73.7%; Pred. No. 2.3e-05;
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 WLMGNILRLFGSMTPAN 19
 Db 115 WLMGNILRLFGSMTPAN 133

RESULT 3
 PAFA_BOVIN
 ID PAFA_BOVIN STANDARD; PRT; 444 AA.


```

Q28017;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLATELET-ACTIVATING FACTOR ACETYLVHDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLVHDROLASE) (PAF 2-ACYLHYDROLASE) (IDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLVHDROLASE) (ESTERASE).
GN PLA2G7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
OX [1]
SEQUENCE FROM N.A.
RN RP
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC CC -|- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -|- TISSUE SPECIFICITY: PLASMA.
CC -|- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANGREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; U34247; AAC48483.1; .
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR000734; Lipase.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 444
FT FT PLATELET-ACTIVATING FACTOR
FT ACETYLVHDROLASE.
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 297 297 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 444 AA; 5013 MW; 97689917BE2F4C38 CRC64;

Query Match 71.3%; Score 72; DB 1; Length 444;
Best Local Similarity 72.2%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WLMGNILRLLFGSMWTPA 18
||:|:| | |||||
Db 115 WLVGKIMGLFGSMWTPA 132

RESULT 4
ID PAFA_MOUSE STANDARD; PRT: 440 AA.
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Q60963;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GS PLA2G7 OR PAFAPAH.
ON Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC
RX TISSUE=Spleen;
RY MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
RA Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H2(O) = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U34277; AAC52274.1; -
CC MGD: MGI:1351327; Pla2g7.
CC DR InterPro: IPR000379; Est_lip_thioest_actsite.
CC DR InterPro: IPR000734; Lipase.
CC DR PROSITE: PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
CC FT SIGNAL 1 21
CC FT CHAIN 22 440
CC FT PLATELET-ACTIVATING FACTOR
CC FT ACETYLHYDROLASE.
CC FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

Query Match 67.3%; Score 68; DB 1; Length 440;
Best Local Similarity 66.7%; Pred. No. 0.00073;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LMGNILRLFLFGSMTPAN 19
Db 115 IVGNILRLFLYGLSLTPAS 132

RESULT 5
PAPA_CAVPA
ID PAPA_CAVPA PRT: 436 AA.

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Q60963;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GS PLA2G7 OR PAFAPAH.
ON Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
RA Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H2O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U34277; AAC52274.1; -
CC MGD: MGI:1351327; Pla2g7.
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR000734; Lipase.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 440
FT PLATELET-ACTIVATING FACTOR
FT ACETYLHYDROLASE.
FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

Query Match 67.3%; Score 68; DB 1; Length 440;
Best Local Similarity 66.7%; Pred. No. 0.00073;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LMGNILRLFLFGSMTPAN 19
:||||| ||:|||||:
Db 115 IVGNILRLFLYGLSLTPAS 132

RESULT 5
PAPA_CAVPO
ID PAPA_CAVPO STANDARD: PRT: 436 AA.

```


RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of *Thermotoga maritima*.";
 RN Nature 399:323-329(1999).
 RN [2].
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS).
 RX MEDLINE=20070293; PubMed=10600747;
 RA Selmer M., Al-Karadaghi S., Hirokawa G., Kaji A., Liljas A.;
 RT "Crystal structure of thermotoga maritima ribosome recycling factor:
 RT A trna mimc.";
 RL Science 286:2349-2352(1999).
 CC -!- FUNCTION: RESPONSIBLE FOR THE RELEASE OF RIBOSOMES FROM MESSENGER
 CC RNA AT THE TERMINATION OF PROTEIN BIOSYNTHESIS. MAY INCREASE THE
 CC EFFICIENCY OF TRANSLATION BY RECYCLING RIBOSOMES FROM ONE ROUND OF
 CC TRANSLATION TO ANOTHER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE RRF FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AE001792; AAD36470.1; -;
 DR PDB; 1DD5; 22-DEC-99.
 DR TIGR; TM1399; -;
 DR InterPro; IPR002661; RRF.
 DR Pfam; PF01765; RRF; 1.
 KW Protein biosynthesis; 3D-structure; Complete proteome.
 SQ SEQUENCE 185 AA; 21513 MW; 626E349B97495852 CRC64;

 Query Match 42.6%; Score 43; DB 1; Length 185;
 Best Local Similarity 61.5%; Pred. No. 4.5;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 GNILRLFGSWTT 16
 Db 95 GNVIRLFPSPPT 107
 ||:|||||
 RESULT 10
 OXRP_HUMAN STANDARD; PRT; 999 AA.
 ID OXRP_HUMAN
 AC Q9Y4L1;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 150 KDA OXYGEN-REGULATED PROTEIN PRECURSOR (ORP150).
 GN ORP150.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Astrocytoma;
 RX MEDLINE=97148579; PubMed=9020069;
 RA Ikeda J., Kaneda S., Kuwabara K., Ogawa S., Kobayashi T.,
 RA Matsumoto M., Yura T., Yanagi H.;
 RT "Cloning and expression of cDNA encoding the human 150 kDa oxygen-
 RT regulated protein, ORP150.";
 RL Biochem. Biophys. Res. Commun. 230:94-99(1997).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=99156921; PubMed=10037731;
 RA Ozawa K., Kuwabara K., Tamatani M., Takatsuji K., Tsukamoto Y.,
 RA Kaneda S., Yanagi H., Stern D.M., Eguchi Y., Tsujimoto Y., Ogawa S.,
 RA Tohyama M.;

RT "150-kDa oxygen-regulated protein (ORP150) suppresses hypoxia-induced
 RT apoptotic cell death.";
 RL J. Biol. Chem. 274:6397-6404(1999).
 CC -!- FUNCTION: HAS A PIVOTAL ROLE IN CYTOPROTECTIVE CELLULAR MECHANISMS
 CC TRIGGERED BY OXYGEN DEPRIVATION, MAY PLAY A ROLE AS A MOLECULAR
 CC CHAPERONE AND PARTICIPATE IN PROTEIN FOLDING.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TISSUES THAT CONTAIN WELL-
 CC DEVELOPED ENDOPLASMIC RETICULUM AND SYNTHESIZE LARGE AMOUNTS OF
 CC SECRETORY PROTEINS. HIGHLY EXPRESSED IN LIVER AND PANCREAS AND
 CC LOWER EXPRESSION IN BRAIN AND KIDNEY. ALSO EXPRESSED IN
 CC MACROPHAGES WITHIN AORTIC ATHEROSCLEROTIC PLAQUES, AND IN BREAST
 CC CANCERS.
 CC -!- INDUCTION: BY HYPOXIA AND ALSO BY 2-DEOXYGLUCOSE OR TUNICAMYCIN.
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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 CC -----
 DR EMBL; U65785; AAC50947.1; -;
 DR MIM; 601746; -;
 DR InterPro; IPR001023; HSP70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PROSITE; PS00297; HSP70_1; FALSE_NEG.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Endoplasmic reticulum; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 999 BY SIMILARITY.
 FT DOMAIN 603 606 150 KDA OXYGEN-REGULATED PROTEIN.
 FT DOMAIN 636 641 POLY-GLU.
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 596 596 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 830 830 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 862 862 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 869 869 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 922 922 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 931 931 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SITE 996 999 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 999 AA; 111335 MW; FCE0F292466AFAB9 CRC64;
 Query Match 41.6%; Score 42; DB 1; Length 999;
 Best Local Similarity 53.3%; Pred. No. 37;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 MGNILRLFGSWTTP 17
 Db 577 LGNTSSSLFGGGTTP 591
 ||:|||||
 RESULT 11
 GUTQ_ECOLI STANDARD; PRT; 321 AA.
 ID GUTQ_ECOLI
 AC P17115; Q46874;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GUTQ PROTEIN.
 GN GUTQ OR SRLQ OR B2708.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

```
RP SEQUENCE OF 3-313 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190542; PubMed=2134185;
RA Yamada M., Yamada Y., Saier M.H. Jr.;
RT "Nucleotide sequence and expression of the gutQ gene within the
RT glucitol operon of Escherichia coli.";
RL DNA Seq. 1:141-145(1990).
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -1- FUNCTION: NOT KNOWN.
CC -1- SUBUNIT: HOMODIMER (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO THE SIS FAMILY. GUTQ/KPSF SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 214.
CC -----
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CC -----
DR EMBL; X51361; CAA35745.1; ALT_FRAME.
DR EMBL; U29579; AAA69217.1; ALT_INIT.
DR EMBL; AE000354; AAC75750.1; ALT_INIT.
DR PIR; S10373; S10373.
DR PIR; A48429; A48429.
DR EcoGene; EG10973; gutQ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001347; SIS.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01380; SIS; 1.
DR ATP-binding; Repeat; CBS domain; Complete proteome.
FT NP_BIND 49 54 ATP (POTENTIAL).
FT DOMAIN 201 255 CBS 1.
FT DOMAIN 267 319 CBS 2.
FT SEQUENCE 321 AA; 34031 MW; 85C31DFBD92F7B7C CRC64;
SQ
Query Match 40.6%; Score 41; DB 1; Length 321;
Best Local Similarity 42.1%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;
QY 1 WLMGNILRLFGSMTPAN 19
DB 254 WLWGG-----GALTTTPVN 266
RESULT 12
ID Y38K_CORSE STANDARD; PRT; 338 AA.
AC Q39635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 38.1 KDA PROTEIN.
OS Corydalis sempervirens (Pink corydalis) (Rock-harlequin).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Fumarioideae; Corydalis.
OX NCBI_TaxID=3464;
RN [1]
RP SEQUENCE FROM N.A.
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RA Schaller A.;
RL Thesis (1991); University of Bochum, Germany.
CC -1- SIMILARITY: BELONGS TO THE THERMONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL; X63595; CAA45139.1; -.
DR HSSP; P00644; ISND.
DR InterPro; IPR000080; SNase.
DR InterPro; IPR002071; Thermonuclease.
DR Pfam; PF00565; SNase; 1.
DR ProDom; PD002274; SNase; 1.
DR SMART; SM00318; SNC; 1.
DR PROSITE; PS01123; TNASE_1; FALSE_NEG.
DR PROSITE; PS01284; TNASE_2; 1.
DR PROSITE; PS00828; TNASE_3; 1.
KW Hypothetical protein; Hydrolase; Nuclease; Endonuclease.
FT ACT_SITE 228 228 BY SIMILARITY.
FT ACT_SITE 236 236 BY SIMILARITY.
FT ACT_SITE 270 270 BY SIMILARITY.
SQ SEQUENCE 338 AA; 38073 MW; 8AD1E39F2CD32507 CRC64;
Query Match 40.6%; Score 41; DB 1; Length 338;
Best Local Similarity 53.3%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 3 MGNILRLFGSMTP 17
DB 1 MGNALRFLYGHCKP 15
RESULT 13
ID YOJA_BACSU STANDARD; PRT; 444 AA.
AC O31862;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PERMEASE IN ODHA-CTPA INTERGENIC REGION.
GN YOJA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=166;
RA Park S.-H., Shin B.-S., Choi S.-K., Ghim S.-Y.;
RT "DNA sequences of a 15.4 kb fragment covering the 181 degree region of
RT the Bacillus subtilis genome."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE GNTF FAMILY OF PERMEASES.
CC -----
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CC -----
DR EMBL; AF026147; AAC17849.1; -.
DR EMBL; Z99114; CABI3843.1; -.
DR Subtilist; BG13554; YOJA.
DR InterPro; IPR003474; GntP_permease.
```

DR Pfam: PF02447; GntP_permease; 1.
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.
FT TRANSMEM 261 281 POTENTIAL.
FT TRANSMEM 305 325 POTENTIAL.
FT TRANSMEM 343 363 POTENTIAL.
FT TRANSMEM 377 397 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
SQ SEQUENCE 444 AA: 4680 MW; 69AEABBA3F6BBFC CRC64;

Query Match 40.6%; Score 41; DB 1; Length 444;
Best Local Similarity 44.4%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTPA 18
| : : ||| | | | |
DB 347 WTIAAVRLCLGSATVAA 364

RESULT 14
GNTP_BACLI STANDARD; PRT: 448 AA.
AC P46832; 1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUCONATE PERMEASE.
GN GNTP.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BGSC5A2;
RX MEDLINE=96051988; PubMed=8535972;
RA Yoshida K.-I., Seki S., Fujita Y.;
RT "Nucleotide sequence and features of the Bacillus licheniformis gnt operon";
RL DNA Res. 1:157-162(1994).
CC -1- PATHWAY: GLUCONATE UTILIZATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE GNTP FAMILY OF PERMEASES.

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CC EMBL: D31631; BAA06503.1; -
DR PIR: J23305; J23305.
DR InterPro: IPR003474; GntP_permease.
DR Pfam: PF02447; GntP_permease; 1.
KW Glucanate utilization; Sugar transport; Transmembrane.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 23 43 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.
FT TRANSMEM 269 289 POTENTIAL.
FT TRANSMEM 302 322 POTENTIAL.

FT TRANSMEM 347 367 POTENTIAL.
FT TRANSMEM 373 393 POTENTIAL.
FT TRANSMEM 428 448 POTENTIAL.
SQ SEQUENCE 448 AA: 46725 MW; A8104496A124D73A CRC64;

Query Match 40.6%; Score 41; DB 1; Length 448;
Best Local Similarity 44.4%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 WLMGNILRLFGSMTPA 18
| : : ||| | | | |
DB 351 WVIAAILRLISLGSATVAA 368

RESULT 15
ANX6_BOVIN STANDARD; PRT: 618 AA.
ID ANX6_BOVIN
AC P79134;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANNEXIN VI (LIPOCORTIN VI) (P68) (P70) (PROTEIN III) (CHROMOBINDIN 20) (67 KDA CALELECTRIN) (CALPHOBINDIN-II) (CPB-II) (FRAGMENT).
GN ANXA6 OR ANX6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Conner C., Creutz C.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=98422308; PubMed=9748523;
RA Avila-Sakar A.J., Creutz C.E., Kretsinger R.H.;
RT "Crystal structure of bovine annexin VI in a calcium-bound state."; Biochim. Biophys. Acta 1387:103-116(1998).
CC -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES.
CC -1- DOMAIN: CONTAINS EIGHT HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
CC -1- PTM: PHOSPHORYLATED IN RESPONSE TO GROWTH FACTOR STIMULATION (BY SIMILARITY).
CC -1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

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CC EMBL: U87539; AAB47570.1; -
DR PDB: 1AVC; 28-JAN-98.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 7.
DR SMART: SM00335; ANX; 8.
DR PROSITE: PS00223; ANNEXIN; 6.
KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation; 3D-structure.
FT NON_TER 1 1
FT REPEAT <1 34 ANNEXIN 1.
FT REPEAT 46 106 ANNEXIN 2.
FT REPEAT 130 190 ANNEXIN 3.
FT REPEAT 205 265 ANNEXIN 4.
FT REPEAT 317 377 ANNEXIN 5.

FT REPEAT 389 449 ANNEXIN 6.
FT REPEAT 478 538 ANNEXIN 7.
FT REPEAT 553 613 ANNEXIN 8.
SQ SEQUENCE 618 AA; 69796 MW; 5571F70F24B8836F CRC64;

Query Match 40.6%; Score 41; DB 1; Length 618;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LMGNILRLFGSMUTPAN 19
| | : | | : | | :
Db 366 LSGDLARLILGLMPPAH 383

Search completed: March 9, 2002, 00:47:36
Job time: 797 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:51 ; Search time 94.88 Seconds
(without alignments)
29.291 Million cell updates/sec

Title: US-09-922-067-4

Perfect score: 101

Sequence: 1 WLMGNILRLFGSMTPAN 19

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	68	67.3	346	11 Q9DB74	Q9db74 mus musculus
2	46	45.5	410	2 Q9KAU8	Q9kau8 bacillus ha
3	45	44.6	417	2 Q9KQ33	Q9kq33 vibrio chol
4	44	43.6	122	5 Q21462	Q21462 caenorhabdi
5	44	43.6	473	5 Q9W1Y9	Q9w1y9 drosophila
6	44	43.6	1040	5 Q9VH04	Q9vh04 drosophila
7	43.5	43.1	301	2 Q9K367	Q9k367 bacillus ce
8	43	42.6	111	6 Q9N0J0	Q9n0j0 bos taurus
9	43	42.6	175	2 Q9XT95	Q9et95 synecococc
10	43	42.6	220	8 Q9B4F4	Q9b4f4 charina bot
11	43	42.6	353	8 Q9TE66	Q9te66 skeletonema
12	43	42.6	353	8 Q9TE64	Q9te64 thalassiosi
13	43	42.6	422	2 P72725	P72725 synecocyst
14	43	42.6	691	2 Q9XDB3	Q9xdb3 staphylococ
15	43	42.6	691	2 Q99TU2	Q99tu2 staphylococ
16	43	42.6	715	5 Q76728	Q76728 trypanosoma
17	43	42.6	836	2 Q9KRL1	Q9krl1 vibrio chol
18	43	42.6	1016	4 Q9NXV1	Q9nxv1 homo sapien
19	42.5	42.1	403	2 Q9RT29	Q9rt29 deinococcus

Q9i4k4 pseudomonas
Q99rd0 staphylococ
Q39134 arabisdopsis
Q9mev0 sclerurus vul
P70051 xenopus lae
Q43600 homo sapien
Q9ln60 arabisdopsis
Q9kew5 bacillus ha
Q9clx4 schizosacch
Q19931 caenorhabdi
Q9r2k2 uncultured
Q44109 drosophila
Q44110 drosophila
Q76996 drosophila
Q77458 drosophila
Q76995 drosophila
Q9ty56 drosophila
Q9yda5 aeropyrum p
Q55675 newcastle d
Q9nrv1 homo sapien
Q9xuq2 caenorhabdi
Q04158 arabisdopsis
Q9plr6 homo sapien
Q9plg3 caenorhabdi
Q64379 arabisdopsis
Q9est4 mus musculu

20 42 41.6 422 2 Q9I4K4
21 42 41.6 452 2 Q99RD0
22 42 41.6 476 10 Q39134
23 42 41.6 605 8 Q9MEV0
24 41.5 41.1 215 13 P70051
25 41 40.6 107 4 Q43600
26 41 40.6 147 10 Q9LN60
27 41 40.6 266 2 Q9KEW5
28 41 40.6 513 3 Q9CLX4
29 41 40.6 1817 5 Q19931
30 40.5 40.1 159 2 Q9R2K2
31 40.5 40.1 235 5 Q44109
32 40.5 40.1 235 5 Q44110
33 40.5 40.1 247 5 Q76996
34 40.5 40.1 247 5 Q77458
35 40.5 40.1 247 5 Q76995
36 40.5 40.1 247 5 Q9TY56
37 40 39.6 123 1 Q9YDA5
38 40 39.6 130 12 Q55675
39 40 39.6 224 4 Q9NRV1
40 40 39.6 233 5 Q9XUQ2
41 40 39.6 255 10 Q04158
42 40 39.6 256 4 Q9PLR6
43 40 39.6 256 5 Q9PLG3
44 40 39.6 257 10 Q64379
45 40 39.6 264 11 Q9EST4

ALIGNMENTS

RESULT 1
ID Q9DB74 PRELIMINARY; . PRT; 346 AA.
AC Q9DB74;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE PHOSPHOLIPASE A2 GROUP VII (PLA2-ACTIVATING FACTOR
DE ACETYLHYDROLASE, PLASMA).
GN PLA2G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauer N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK005158; BAB23849.1; -
DR MGD: MGI:1351327; Pla2g7.
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR000734; Lipase.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SQ SEQUENCE 346 AA; 38967 MW; D68A2A128402E554 CRC64;

Query Match 67.3%; Score 68; DB 11; Length 346;
Best Local Similarity 66.7%; Pred. No. 0.0027;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMGNILRLFLGSMTPAN 19
:||||| :|||:|||||
Db 115 IVGNILHLGLSLTPAS 132

RESULT 2
Q9KAU8 PRELIMINARY; PRT; 410 AA.
AC Q9KAU8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SPORE GERMINATION PROTEIN I.
GN GERA OR BH2188.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.*;
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001514; BAB05907.1; -;
KW Complete proteome.
SQ SEQUENCE 410 AA; 46029 MW; 20E5722AB95AE46D CRC64;

Query Match 45.5%; Score 46; DB 2; Length 410;
Best Local Similarity 47.8%; Pred. No. 15;
Matches 11; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 WLMGNILRL-----FGSMTP 17
||||| :|||
Db 213 WLMGSALRLRLTSPFFIGFVLTP 235

RESULT 3
Q9KQ33 PRELIMINARY; PRT; 417 AA.
AC Q9KQ33;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE URACIL PERMEASE.
GN VC2171.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Emmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004288; AAF95316.1; -;
DR TIGR; VC2171; -;
DR InterPro; IPR000444; xan_ur_permease.
DR Pfam; PF00860; xan_ur_permease; 1.
DR PROSITE; PS01116; XANTH_URACIL_PERMEASE; 1.
KW Complete proteome.
SQ SEQUENCE 417 AA; 43282 MW; 743A369DC814B7B9 CRC64;

Query Match 44.6%; Score 45; DB 2; Length 417;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LMGNILRLFLGSMTP 16
:||| :|||||
Db 323 VMGGIMILLFGSTAT 337

RESULT 4
Q21462 PRELIMINARY; PRT; 122 AA.
ID Q21462
AC Q21462;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE COSMID M02D8.
GN M02D8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wooldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RN Nature 368:32-38(1994).
RP [2]
RP SEQUENCE FROM N.A.
RA Miller N.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBDJ databases.
DR EMBL; U41034; AAA82380.1; -;
SQ SEQUENCE 122 AA; 13773 MW; 29ACC97CE1016D98 CRC64;

Query Match 43.6%; Score 44; DB 5; Length 122;
Best Local Similarity 44.4%; Pred. No. 9.5;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 WLMGNILRLFLGSMTPA 18
| :| :| :| :|
Db 73 WVDGDIIRLVFNNSPTGA 90

RESULT 5
Q9W1Y9

ID Q9W1Y9 PRELIMINARY; PRT; 473 AA.
 AC Q9W1Y9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG3649 PROTEIN.
 GN CG3649.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champagne M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA DePablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of Drosophila melanogaster.
 RL Science 287:2185-2195(2000).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
 DR EMBL; AE003458; AAF46912.1;
 DR Flybase; FBgn0034785; CG3649.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane.
 SQ SEQUENCE 473 AA; 52199 MW; 904F761C873FD6FF CRC64;

Query Match 43.6%; Score 44; DB 5; Length 473;
 Best Local Similarity 53.8%; Pred. No. 38;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 3 MGNILRLFGSMT 15
 Db 421 LGNMLYFGQMT 433
 :||: |||||

RESULT 6
 Q9VH04 PRELIMINARY; PRT; 1040 AA.
 AC Q9VH04;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CG11871 PROTEIN.
 GN CG11871.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA DePablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of Drosophila melanogaster.
 RL Science 287:2185-2195(2000).
 CC EMBL; AE003458; AAF54517.1;
 DR Flybase; FBgn0037805; CG11871.
 SQ SEQUENCE 1040 AA; 111252 MW; E63B68169E1C4896 CRC64;

Query Match 43.6%; Score 44; DB 5; Length 1040;
 Best Local Similarity 56.2%; Pred. No. 85;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 MGNILRLFGSMTTPA 18
 Db 95 VGDICLLMGTTATTPA 110
 :||: |||||

RESULT 7
 Q9K367 PRELIMINARY; PRT; 301 AA.
 ID Q9K367

Q9K367;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE YNDD PROTEIN (PUTATIVE SPORE GERMINATION PROTEIN) (FRAGMENT).
GN YNDD.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 14579;
RA Oktad O.A., Agasse H., Lereclus D., Kolsto A.B.;
FT "20 kb DNA sequence surrounding the hblA hemolytic enterotoxin locus
from Bacillus cereus ATCC 14579.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 14579;
RA MEDLINE-20055637; PubMed=10589720;
FT "Sequence analysis of three Bacillus cereus loci under P1CR-regulated
genes encoding degradative enzymes and enterotoxin.";
RL Microbiology 145:3129-3138(1999).
DR EMBL; AJ007795; CAB6936.1; -;
DR EMBL; AJ237785; CAB69787.1; -;
FT NON_TER 1
SQ SEQUENCE 301 AA; 33612 MW; 37650BEDA9603D2 CRC64;

Query Match 43.1%; Score 43.5; DB 2; Length 301;
Best Local Similarity 47.8%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 5; Indels 5; Gaps 1;
Qy 1 WLMGNILRL-----FGSMWTPA 18
|||:||||| | | | |
Db 93 WLPGLTLLRLRLFWMTAFVSLFAPA 115

RESULT 8
Q9N0J0 ID Q9N0J0 PRELIMINARY; PRT; 111 AA.
AC Q9N0J0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANGIOTENSIN RECEPTOR 2 (FRAGMENT).
GN AT2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Berisha B.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Acosta T., Berisha B., Ozawa T., Sato K., Schams D., Miyamoto A.;
FT "Evidence for local endothelin-angiotensin atrial natriuretic peptide
system in bovine mature follicles in vitro: effects on steroid
hormones and prostaglandin secretion.";
RL Biol. Reprod. 61:1419-1425(1999).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ277986; CAB92128.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.

DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 13102 MW; 9E8A81D3D580A601 CRC64;

Query Match 42.6%; Score 43; DB 6; Length 111;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WLMGNILRLFGSMWTT 16
|||:|||||
Db 17 WLFPGVMCKLFGSFLT 32

RESULT 9
Q9ET95 ID Q9ET95 PRELIMINARY; PRT; 175 AA.
AC Q9ET95;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME C550 LIKE PROTEIN.
GN PSBV2.
OS Synechococcus vulcanus, and
OS Thermosynechococcus elongatus.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32053; 146786;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.vulcanus, and T.elongatus;
RA Katoh H., Itoh S., Shen J., Ikeuchi M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-S.vulcanus, and T.elongatus;
RA "CLONING OF THE GENES FOR CYTOCHROME C550 AND A C550-LIKE PROTEIN FROM
THE THERMOPHILIC CYANOBACTERIUM Synechococcus elongatus.";
RL Plant Cell Physiol. 40:89-89(1999).
DR EMBL; AB052598; BAB20064.1; -;
DR EMBL; AB052597; BAB20060.1; -;
DR InterPro: IPR000345; Cyt_c550.
DR InterPro: IPR003218; Cyt_c550.
DR ProDom: PD010841; Cyt_c550; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 175 AA; 19118 MW; FB95EE348651C44 CRC64;

Query Match 42.6%; Score 43; DB 2; Length 175;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 WLMGNILRLFGSMWTPA 18
|||:||||| | | | |
Db 13 WLCGGLLILLGLWTIAPA 30

RESULT 10
Q9B4F4 ID Q9B4F4 PRELIMINARY; PRT; 220 AA.
AC Q9B4F4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT 4 (FRAGMENT).
OS Charina bottae.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Boidae; Boidae;

OC Charina.
RN NCBI_TaxID=51858;
RX SEQUENCE FROM N.A.

RA MEDLINE=21097362; PubMed=11161758;
RQ Rodriguez-Robles J.A., Stewart G.R., Papenfuss T.J.;
RT Mitochondrial DNA-Based Phylogeography of North American Rubber Boas,
RL Charina bottae (Serpentes: Boidae).";
RM Mol. Phylogenet. Evol. 18:227-237(2001).
DR EMBL; AF302976; AAK19214.1; -;
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 220 AA; 24488 MW; 46B28E57993399A5 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 220;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 WLMGNILRLLF 11
DB 125 WLMGNILMIAF 135

RESULT 11

ID Q9TE66 PRELIMINARY; PRT; 353 AA.
AC Q9TE66;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COXI.
OS Skeletonema costatum.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Thalassiosirophyceae; Thalassiosirales; Skeletonemataceae;
OC Skeletonema.
OX NCBI_TaxID=2843;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCAP 1077-1B;
RA Ehara M., Inagaki Y., Watanabe K.I., Ohama T.;
RT "Phylogenetic analysis of diatom cox1 genes and implications of
fluctuating GC content on mitochondrial genetic code evolution.";
RL Curr. Genet. 0:0-0(1999).
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICCYTOCHROME C.
CC -!- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AB020227; BAA86612.1; -;
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PROSITE; PS00077; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38158 MW; F107054A59A65521 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 353;
Best Local Similarity 55.6%; Pred. No. 41;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
OY 1 WLMGNILRLLFSGMTTPA 18
DB 90 WLLPPSLLLLFASMLTEA 107

RESULT 12

ID Q9TE64 PRELIMINARY; PRT; 353 AA.
AC Q9TE64;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COXI OR COX1.
OS Thalassiosira nordenskioldii.
OG Mitochondrion.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Thalassiosirophyceae; Thalassiosirales; Thalassiosiraceae;
OC Thalassiosira.
OX NCBI_TaxID=83372;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCMP992;
RA Ehara M., Inagaki Y., Watanabe K.I., Ohama T.;
RT "Phylogenetic analysis of diatom cox1 genes and implications of
fluctuating GC content on mitochondrial genetic code evolution.";
RL Curr. Genet. 0:0-0(1999).
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICCYTOCHROME C.
CC -!- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AB020229; BAA86614.1; -;
DR EMBL; AB038235; BAB21616.1; -;
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38158 MW; F107054A59A65521 CRC64;

Query Match 42.6%; Score 43; DB 8; Length 353;
Best Local Similarity 55.6%; Pred. No. 41;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 WLMGNILRLLFSGMTTPA 18
DB 90 WLLPPSLLLLFASMLTEA 107

RESULT 13
P72725

P72725 PRELIMINARY; PRT; 422 AA.
AC P72725; 42.6%; Score 43; DB 2; Length 691;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 45.7 KDA PROTEIN.
GN SLR1411.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90900; BAA16733.1; -.
DR InterPro; IPR002822; DUF111.
DR Pfam; PF01969; DUF111; 1.
DR ProDom; PD018127; DUF111; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 422 AA; 45731 MW; 38161945A217A492 CRC64;

Query Match 42.6%; Score 43; DB 2; Length 422;
Best Local Similarity 52.9%; Pred. No. 50;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 MGNTLRLLFGSWTPAN 19
Db 238 LANILRLWIGTEITPHN 254

RESULT 14
Q9XDB3 PRELIMINARY; PRT; 691 AA.
AC Q9XDB3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PENICILLIN-BINDING PROTEIN BPP2B (PENICILLIN-BINDING PROTEIN 3).
GN BPPF OR BPP3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ISP3;
RX MEDLINE=99318581; PubMed=10390206;
RA Komatsuzawa H., Choi G.H., Ohta K., Sugai M., Tran M.T., Suganaka H.;
RT "Cloning and characterization of a gene, bppf, encoding a new
RT penicillin-binding protein, BPP2B, in Staphylococcus aureus.";
RL Antimicrob. Agents Chemother. 43:1578-1583(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=COL;
RX MEDLINE=20115552; PubMed=10648534;
RA Pinho M.G., Lencastre H., Tomasz A.;
RT "Cloning, Characterization, and Inactivation of the Gene bppC,
RT Encoding Penicillin-Binding Protein 3 of Staphylococcus aureus.";
RL J. Bacteriol. 182:1074-1079(2000).
DR EMBL; AF098801; AAD43176.1; -.
DR EMBL; AJ243120; CAB72261.1; -.
DR InterPro; IPR001460; Transpeptidase.
DR Pfam; PF00905; Transpeptidase; 1.
SQ SEQUENCE 691 AA; 77238 MW; 4D9D2EA0DCCB3691 CRC64;

Query Match 42.6%; Score 43; DB 2; Length 691;
Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILRLFGSWTPA 18
Db 235 GDTLRGIFGVSTPA 249

RESULT 15
Q99TU2 PRELIMINARY; PRT; 691 AA.
AC Q99TU2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PENICILLIN-BINDING PROTEIN 3.
GN BPP3 OR SAL381.
OS Staphylococcus aureus subsp. aureus N315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ul Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003134; BAB42644.1; -.
KW Complete proteome.
SQ SEQUENCE 691 AA; 77224 MW; 4D9F5A0DCCFED91 CRC64;

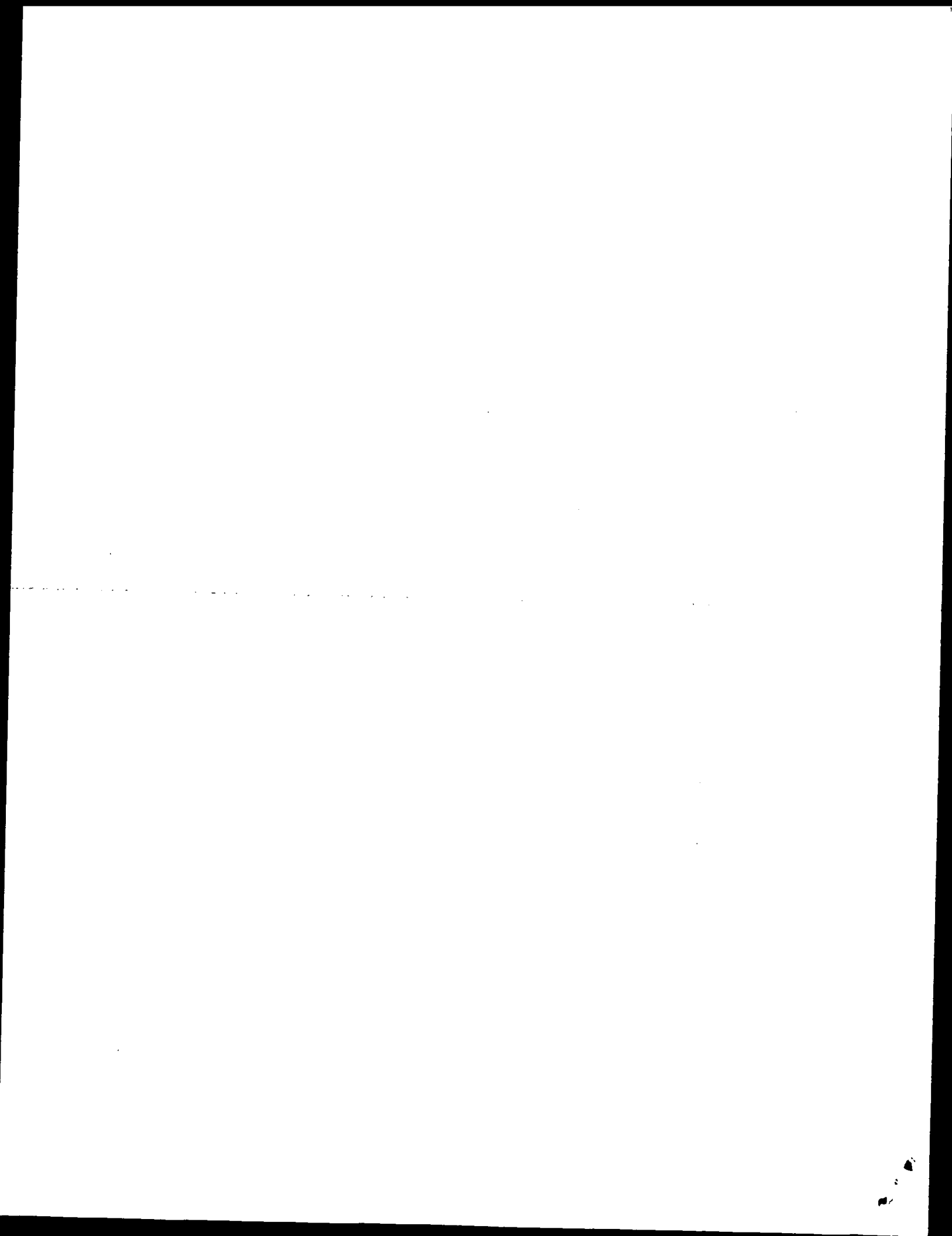
Query Match 42.6%; Score 43; DB 2; Length 691;
Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GNILRLFGSWTPA 18
Db 235 GDTLRGIFGVSTPA 249

Search completed: March 9, 2002, 00:46:53
Job time: 829 sec

us-09-922-067-4.rspt

Mon Mar 11 10:02:11 2002



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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 20:38:16 ; Search time 1981.93 Seconds
(without alignments)
11328.685 Million cell updates/sec

Title: US-09-922-067-9
Perfect score: 1361
Sequence: 1 TCAGAGACTAAGCTGAACT.....AGGAATAGAGAAATACAATT 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues 2944280
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_om.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htgo_hum.*
- 31: em_htgo_inv.*
- 32: em_htgo_rod.*
- 33: em_htg_hum.*
- 34: em_htg_inv.*
- 35: em_htg_rod.*
- 36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1361	100.0	1361	6	A41956	A41956 Sequence 9
2	1361	100.0	1361	6	AR080658	AR080658 Sequence
3	1361	100.0	1361	6	AR084987	AR084987 Sequence
4	1361	100.0	1361	6	AR125358	AR125358 Sequence
5	1361	100.0	1361	6	AX006795	AX006795 Sequence
6	1361	100.0	1561	9	HSU24577	U24577 Human LDL-p
7	1359.4	99.9	1505	9	HSU20157	U20157 Human plate
8	1359.4	99.9	1520	6	AR1377	AR1377 Sequence 7
9	1359.4	99.9	1520	6	AR064404	AR064404 Sequence
10	1359.4	99.9	1520	6	AR083755	AR083755 Sequence
11	1359.4	99.9	1520	6	AR141150	AR141150 Sequence
12	1359.4	99.9	1520	6	AR142503	AR142503 Sequence
13	1359.4	99.9	1520	6	I23385	I23385 Sequence 7
14	1359.4	99.9	1520	6	I49901	I49901 Sequence 7
15	1359.4	99.9	1520	6	I60362	I60362 Sequence 7
16	1359.4	99.9	1520	6	I85595	I85595 Sequence 7
17	1162.4	85.4	1335	6	AR1400	AR1400 Sequence 30
18	1162.4	85.4	1335	6	AR064425	AR064425 Sequence
19	1162.4	85.4	1335	6	AR083776	AR083776 Sequence
20	1162.4	85.4	1335	6	AR141171	AR141171 Sequence
21	1162.4	85.4	1335	6	AR142524	AR142524 Sequence
22	1162.4	85.4	1335	6	I60383	I60383 Sequence 30
23	1049.6	77.1	1506	4	BTU34247	U34247 Bovine plas
24	1049.6	77.1	1533	6	AR1393	AR1393 Sequence 23
25	1049.6	77.1	1533	6	AR064419	AR064419 Sequence
26	1049.6	77.1	1533	6	AR083770	AR083770 Sequence
27	1049.6	77.1	1533	6	AR141165	AR141165 Sequence
28	1049.6	77.1	1533	6	AR142518	AR142518 Sequence
29	1049.6	77.1	1533	6	I60377	I60377 Sequence 23
30	1043.2	76.6	2191	6	AR1392	AR1392 Sequence 22
31	1043.2	76.6	2191	6	AR064418	AR064418 Sequence
32	1043.2	76.6	2191	6	AR083769	AR083769 Sequence
33	1043.2	76.6	2191	6	AR141164	AR141164 Sequence
34	1043.2	76.6	2191	6	AR142517	AR142517 Sequence
35	1043.2	76.6	2191	6	I49915	I49915 Sequence 22
36	1043.2	76.6	2191	6	I60376	I60376 Sequence 22
37	1043.2	76.6	2191	6	I85609	I85609 Sequence 22
38	1043.2	76.6	2222	4	CFU34246	U34246 Dog plasma
39	808.2	58.4	1669	10	BC010726	BC010726 Mus muscu
40	796.8	58.5	2909	10	D67037	D67037 Guinea pig
41	783.6	57.6	1494	6	AR1391	AR1391 Sequence 21
42	783.6	57.6	1494	6	AR064417	AR064417 Sequence
43	783.6	57.6	1494	6	AR083768	AR083768 Sequence
44	783.6	57.6	1494	6	AR141163	AR141163 Sequence
45	783.6	57.6	1494	6	AR142516	AR142516 Sequence

ALIGNMENTS

RESULT 1

A41956
LOCUS A41956 1361 bp DNA
DEFINITION Sequence 9 from Patent WO9500649.
ACCESSION A41956
VERSION A41956.1 GI:2297493
KEYWORDS .
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphree,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S.,
TITLE Lawrence,G.W. and Rice,S.O.
JOURNAL LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 2?, INHIBITORS THEREOF AND
USE OF THE SAME IN DIAGNOSIS AND THERAPY
COMMENT Patent: WO 9500649-A 9 05-JAN-1995;
SMITHKLINE BEECHAM PLC (GB)
FEATURES Other publication JP 8500740T 960130.
source location/Qualifiers
1 .1361

Db	721	ATGTTCCCAAGCTCTCAGTCTGATTCTTTGACATTGATCATGGAAAGCCAGTGAGAATGC	780
Qy	781	ATTAGATTTTAAAGTTTGATATGGAAACAACTGAAGGACTCTATTGATAGCGGAAAAATAGC	840
Db	781	ATTAGATTTTAAAGTTTGATATGGAAACAACTGAAGGACTCTATTGATAGCGGAAAAATAGC	840
Qy	841	AGTAATTGGACATCTTTTTTGTTGGGAGCAACGGTTATTCCAGACTCTTAGTGAAGATCAGAG	900
Db	841	AGTAATTGGACATCTTTTTTGTTGGGAGCAACGGTTATTCCAGACTCTTAGTGAAGATCAGAG	900
Qy	901	ATTCCAGATGTGGTATTGGCCCTGGATGCATGATGTTCCACATGGGTGATGAAGTATATTTC	960
Db	901	ATTCCAGATGTGGTATTGGCCCTGGATGCATGATGTTCCACATGGGTGATGAAGTATATTTC	960
Qy	961	CAGAATTCTCCAGGCCCTCTTTTTTTATTCAACTCTGCAATATTTCCTGAATATCTCGCTAAATAT	1020

QY	1021	CATAAAATGAAAAATGCTACTCACTCGATGATAAGAAAAAGATGATTACAATCAGGGG	1080
Db	1021	CATAAAATGAAAAATGCTACTCACTCGATGATAAGAAAAAGATGATTACAATCAGGGG	1080
QY	1081	TTAGTCCACAGAAATTTTGTCTGACTTCACATTTTGGCAAAATTAATTTGGACACAT	1140
Db	1081	TTAGTCCACAGAAATTTTGTCTGACTTCACATTTTGGCAAAATTAATTTGGACACAT	1140
QY	1141	GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAGCTTC	1200
Db	1141	GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAGCTTC	1200
QY	1201	ATTAGCATCTTTCACAAAAGCAATTTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
Db	1201	ATTAGCATCTTTCACAAAAGCAATTTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
QY	1261	GATTGAAGGAGATGATGAGAATCTTATTCCAGGACCACCAACATTAACACAACCAATCAACA	1320
Db	1261	GATTGAAGGAGATGATGAGAATCTTATTCCAGGACCACCAACATTAACACAACCAATCAACA	1320
QY	1321	CATCATGCTTACAGAACTCTTCAGGAATAGAGAAATACAAAT	1361
Db	1321	CATCATGCTTACAGAACTCTTCAGGAATAGAGAAATACAAAT	1361
RESULT 2			
LOCUS	AR080658	1361 bp	DNA
DEFINITION	Sequence 9 from patent US 5968818.		PAT
ACCESSION	AR080658		
VERSION	AR080658.1	GI:10007388	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1361)		
AUTHORS	Gloger,I.Simon, Lawrence,G.MarkProuse and Rice,S.QuentynJohn.		
TITLE	Lipoprotein associated phospholipase A2, inhibitors thereof and use		
JOURNAL	of the same in diagnosis and therapy		
FEATURES	Patent: US 5968818-A 9 19-OCT-1999;		
source	Location/Qualifiers		
	1..1361		
	/organism="unknown"		
BASE COUNT	417 a 273 c 278 g 393 t		
ORIGIN			
Query Match 100.0%; Score 1361; DB 6; Length 1361;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	TGAGAGACTAAGCTGAACCTGCTGCTCAGCTGCCAAGATGCTGCCACCAAAATTTGCATGT	60

QY	61	GC	TTTCTG	CCCTCG	CGGCTGC	CTGGCTGTGGT	TATCCT	TTTGACTGG	CAATACATAA	120
Db	61	GC	TTTCTG	CCCTCG	CGGCTGC	CTGGCTGTGGT	TATCCT	TTTGACTGG	CAATACATAA	120
QY	121	TC	CTGTTC	CCCATATG	AAATCAT	CAGCATGGG	TCAACAAATACA	AGTACTGATGG	CTGC	180
Db	121	TC	CTGTTC	CCCATATG	AAATCAT	CAGCATGGG	TCAACAAATACA	AGTACTGATGG	CTGC	180
QY	181	TG	CAAGCTTT	TG	CCAACTAA	ATCC	CCGCGGAAATGG	CGCTTATTCG	TTGGTTGTAC	240
Db	181	TG	CAAGCTTT	TG	CCAACTAA	ATNA	TCCCGCGGAAATGG	CGCTTATTCG	TTGGTTGTAC	240
QY	241	AG	ACTTAATG	TTTGAT	CACACTAA	TAAAGG	GCACCTCTCTG	CGTTATAT	TATTCATPCCA	300
Db	241	AG	ACTTAATG	TTTGAT	CACACTAA	TAAAGG	GCACCTCTCTG	CGTTATAT	TATTCATPCCA	300
QY	301	AG	ATAATGAT	CGCCTTG	ACACCC	TTTGAT	CCCAATAA	AGAAATAT	TTTGGGCTTAG	360
Db	301	AG	ATAATGAT	CGCCTTG	ACACCC	TTTGAT	CCCAATAA	AGAAATAT	TTTGGGCTTAG	360
QY	361	CA	AAATTTCT	TGGA	CACACTGG	CTTATG	GGCAACATTTG	AGGTTACT	CTTTGGTTCAAT	420
Db	361	CA	AAATTTCT	TGGA	CACACTGG	CTTATG	GGCAACATTTG	AGGTTACT	CTTTGGTTCAAT	420
QY	421	GAC	AACTCCTG	CAACTG	GAATCC	CTCTG	AGGCGCTG	TGAAAAAT	TATCCACTTGTGT	480
Db	421	GAC	AACTCCTG	CAACTG	GAATCC	CTCTG	AGGCGCTG	TGAAAAAT	TATCCACTTGTGT	480
QY	481	TTTT	TCTCAT	GGTCTT	GGGCATTC	AGACACTTT	TATCTG	CTATTTGG	CAATTCACCTGGC	540
Db	481	TTTT	TCTCAT	GGTCTT	GGGCATTC	AGACACTTT	TATCTG	CTATTTGG	CAATTCACCTGGC	540
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QY	601	CT	ATTTCA	AGGACCA	ATCTG	CTGAG	AAATAGGG	GACAGTCTT	TGGCTCTACTTTAGAAC	660
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QY	661	CCT	GAACAAG	GAGGAG	CACACATAT	AG	AAATGAC	AGGTACG	CGCAAGACAAAGA	720
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QY	781	ATT	AGATTTAA	AGTTT	GATATG	GAACAA	CTGAAG	GCCTATTG	TATAGGGAAAAATAGC	840
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QY	841	AG	TATTTGG	CACATCTT	TTTGGT	TGGACACG	GTATT	CAGACTCT	TAGTCAAGATCAGAG	900
Db	841	AG	TATTTGG	CACATCTT	TTTGGT	TGGACACG	GTATT	CAGACTCT	TAGTCAAGATCAGAG	900
QY	901	AT	TCAGATGT	GTGATT	TG	CCCTGG	ATGCTG	GTATTTCC	ACTGGGTGAAGTATATTC	960
Db	901	AT	TCAGATGT	GTGATT	TG	CCCTGG	ATGCTG	GTATTTCC	ACTGGGTGAAGTATATTC	960
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[illegible]

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Best Local Similarity	100.0%	pred. No. 0:		
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DEFINITION Sequence 9 from patent US 6177257.
ACCESSION AR125358
VERSION AR125358.1 GI:14111420
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)

AUTHORS Macphree, C. Houston, Tew, D. Graham, Southan, C. Donald, Hickey, D. MaryBernadette, Gloger, I. Simon, Lawrence, G. MarkProuse and Rice, S. QuentynJohn.
TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use of the same in diagnosis and therapy
JOURNAL Patent: US 6177257-A 9 23-JAN-2001;
FEATURES Location/Qualifiers
source 1..1361
BASE COUNT 417 a 273 c 278 g 393 t
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 ACCESSION U24577
 VERSION U24577.1 GI:1314245
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 SOURCE human.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1561)
 Tew,D.G., Southan,C., Rice,S.O., Lawrence,M.P., Li,H., Boyd,H.F.,
 Moores,K., Gloger,I.S. and Macphree,C.H.,
 Purification, properties, sequencing, and cloning of a
 lipoprotein-associated, serine-dependent phospholipase involved in
 the oxidative modification of low-density lipoproteins
 Arterioscler. Thromb. Vasc. Biol. 16 (4), 591-599 (1996)
 96197208
 2 (bases 1 to 1561)
 Rice,S.O.J.
 Direct Submission
 Submitted (10-APR-1995) Simon O.J. Rice, SmithKline Beecham
 Pharmaceuticals, New Frontiers Science Park North, Third Avenue,
 Harlow, Essex CM195AW, UK
 On May 16, 1996 this sequence version replaced gi:790655.
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ACCESSION U20157
VERSION U20157.1 GI:780132
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AUTHORS Tjoelker,L.W., Wilder,C., Eberhardt,C., Stafforini,D.M.,
Dietsch,G., Schlimp,B., Hooper,S., Trong,H., Cousens,L.S.,
Zimmerman,G.A., Yamada,Y., McIntyre,T.M., Prescott,S.M. and
Gray,P.W.
TITLE Anti-inflammatory properties of a platelet-activating
factor acetylhydrolase
JOURNAL Nature 374 (6522), 549-553 (1995)
MEDLINE 95214779
REFERENCE 2 (bases 1 to 1505)
AUTHORS Tjoelker,L.W.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1995) Larry W. Tjoelker, ICOS Corporation, 22021
20th Ave., S.E., Bothell, WA 98021, USA
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Db 1025 ATTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1084
Qy 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1144

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JOURNAL Patent: US 597308-A 7 02-NOV-1999;

FEATURES Location/Qualifiers

1. 1520

/organism="unknown"

BASE COUNT 453 a 311 c 333 g 423 t

ORIGIN

Query Match 99.9%; Score 1359.4; DB 6; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11

ARI41150

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local

Matches 1360;

Qy 1

Db 125

Qy 61

Db 185

Qy 121

Db 245

Qy 181

Db 305

Qy 961

Db 1024

Qy 960

Db 960

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Db 960

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Db 960

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DEFINITION Sequence 7 from patent US 6203790.
ACCESSION AR142503
VERSION AR142503.1 GI:15103789
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1520)
AUTHORS Cousins, L.S., Eberhardt, C.D., Gray, P., Trong, H. Le, Tjoelker, L.W. and Wilder, C.L.
TITLE Platelet-activating factor acetylhydrolase
JOURNAL Patent: US 6203790-A 7 20-MAR-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 453 a 311 c 333 g 423 t
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Query Match 99.9%; Score 1359.4; DB 6; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 14
LOCUS 149901 1520 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5641669.
ACCESSION 149901
VERSION 149901.1 GI:2472121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1520)
AUTHORS Cousins,B.S., Eberhardt,C.D., Gray,P., Trong,H.Le, Tjoelker,L.W.
and Wilder,C.L.
TITLE Platelet-activating factor acetylhydrolase
JOURNAL Patent: US 5641669-A 7 24-JUN-1997;
FEATURES
source Location/Qualifiers
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BASE COUNT 453 a 311 c 333 g 423 t
ORIGIN

Query Match 99.98; Score 1359.4; DB 6; Length 1520;
Best local Similarity 99.98; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATCT 60
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RESULT 15
LOCUS 160362 1520 bp DNA PAT 07-OCT-1997

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Search completed: March 8, 2002, 22:37:36
Job time: 7160 sec

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Job time: 7160 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 22:03:27 ; Search time 174.17 Seconds
(without alignments)
6699.315 Million cell updates/sec

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Perfect score: 1361
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1359.4	99.9	1520	18	Human platelet-act
5	1359.4	99.9	1520	18	Human plasma plate
6	1359.4	99.9	1520	19	Human plasma plate
7	1359.4	99.9	1520	20	Human PAF-AH codin
8	1359.4	99.9	1520	20	CDNA encoding plas
9	1359.4	99.9	1520	21	Human platelet-act
10	1359.4	99.9	1520	21	Human PAF-AH cdna
11	1359.4	99.9	1520	21	Human PAF-AH cdna

12	1359.4	99.9	1520	22	AA04143	Human plasma plate
13	1359.4	99.9	1520	22	AAC89057	Platelet-activatin
14	1357.4	99.7	1520	22	AAT63701	CDNA encoding plat
15	1247.8	91.7	1320	22	AA04169	Mouse-Human plasma
16	1172.6	86.2	1320	22	AA04168	Mouse-Human plasma
17	1162.4	85.4	1335	22	AAT87072	Human platelet-act
18	1162.4	85.4	1335	21	AA10885	Synthetic PAF-AH c
19	1162.4	85.4	1335	21	AA224261	Human PAF-AH cdna
20	1162.4	85.4	1335	22	AA04165	Human plasma plate
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25	1049.6	77.1	1533	21	AA59594	Bovine PAF-AH codi
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28	1049.6	77.1	1533	22	AA04158	Platelet-activatin
29	1049.6	77.1	1533	22	AAC89072	Canine platelet-act
30	1043.2	76.6	2191	16	AAQ87949	Canine platelet-act
31	1043.2	76.6	2191	18	AAT87065	Canine plasma plat
32	1043.2	76.6	2191	18	AAT80581	Canine PAF-AH codi
33	1043.2	76.6	2191	19	AAT96129	Canine plasma plat
34	1043.2	76.6	2191	20	AA08477	Canine plasma plat
35	1043.2	76.6	2191	20	AAV08551	Canine PAF-AH codi
36	1043.2	76.6	2191	21	AA59593	Canine PAF-AH codi
37	1043.2	76.6	2191	21	AAA10878	CDNA encoding plat
38	1043.2	76.6	2191	21	AA224254	Canine PAF-AH nucl
39	1043.2	76.6	2191	21	AA04157	Canine PAF-AH cdna
40	1043.2	76.6	2191	22	AAC89071	Platelet-activatin
41	1043.2	76.6	2191	22	AAC89071	Murine platelet-act
42	783.6	57.6	1494	16	AAQ87948	Mouse platelet-act
43	783.6	57.6	1494	18	AAT87064	Mouse plasma plate
44	783.6	57.6	1494	18	AAT80580	Mouse plasma plate
45	783.6	57.6	1494	19	AAT96128	Mouse plasma plate

ALIGNMENTS

RESULT 1
AAQ81780
ID AAQ81780 standard; cdna; 1361 BP.
XX
AC AAQ81780;
XX
DT 18-AUG-1995 (first entry)
XX
DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
XX
KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;
KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic;
XX ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 38..1357
XX /*tag= a
XX
XX WO9500649-A.
XX
XX 05-JAN-1995.
XX
XX 24-JUN-1994; 94WO-GH01374.
XX
XX 25-JUN-1993; 93GB-0013144.
XX
XX 11-JAN-1994; 94GB-0000413.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Gloger JS, Hickey DMB, Lawrence GMP, Macphee CH;
XX Rice SQJ, Southan CD, Tew DG;
XX

DR WPI; 1995-052086/07.
 XX P-PSDB; AAR64928.
 PT Purified lipoprotein associated phospholipase A2 - used to
 PT develop prods. for diagnosis and therapy, partic. inhibitors for
 PT treatment of atherosclerosis
 XX
 PS Claim 8; Page 19; 29pp; English.
 XX
 CC This sequence encodes an enzyme which may be used in a method of
 CC screening compounds to identify those compounds which inhibit
 CC Lp-PLA2 which involves contacting isolated Lp-PLA2 with a test
 CC compound and measuring the rate of turnover of an enzyme substrate
 CC as compared with the rate of turnover in the absence of the test
 CC compound.
 XX
 SQ Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 other;

Query Match 100.0%; Score 1361; DB 16; Length 1361;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCACCCCAATTCGATGT 60
 DB 1 tgagagactaagctgaacactgctgctcagctcccaagatggtgcaccccaattcgatgt 60
 QY 61 GCTTTTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 61 gcttttctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120
 QY 121 TCCTGTGGCCATATGAATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180
 DB 121 tcctgtggccatatagaatcatcatcatcatcatcatcatcatcatcatcatcatcatcat 180
 QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGAAATGGGCCCTTATTCCTGCTGCTGCTGCTGCT 240
 DB 181 tgcaagctttggccaaactaaatcccgggaaatgggcccttatttcctgctgctgctgctg 240
 QY 241 AGACTTAATGTTGATCACACTAATAAGGCGACCTCTTCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 agacttaatgttgatcacactaataaaggcgacctcttctgctgctgctgctgctgctgct 300
 QY 301 AGATAATGATCCCTTGACACCTTTGGATCCCAATAAAGATATTTTGGGCTCTTAG 360
 DB 301 agataatgatcccttgacacctttggatcccaataaagatattttgggctcttag 360
 QY 361 CAAATTTCTTGGACACACTGGCTTATGGGCAACATTTTGAGCTTACTCTTTGCTTCAAT 420
 DB 361 caaatTTCTTGGACACACTGGCTTATGGGCAACATTTTGAGCTTACTCTTTGCTTCAAT 420
 QY 421 GACAACTCTGCAACTGGAATTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
 DB 421 gacaaCTCTGCAACTGGAATTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
 QY 481 TTTTCTCATGCTTGGGCAATTCAGGACACTTTATTTCTGCTATTTGCTATTCACCTGGC 540
 DB 481 ttttctcatgcttgggcaatTCAGGACACTTTATTTCTGCTATTTGCTATTCACCTGGC 540
 QY 541 ATCTCATGGGTTTATGTTGCTGTGTAGACACAGATAGATCTGCAATCTGCAACTTA 600
 DB 541 atctcatGGGTTTATGTTGCTGTGTAGACACAGATAGATCTGCAATCTGCAACTTA 600
 QY 601 CTATTTCAGGACCAATCTGCTGCAAGATATAGGGGACAAAGTCTTGCTCTACCTTAGAAC 660
 DB 601 ctattTCAGGACCAATCTGCTGCAAGATATAGGGGACAAAGTCTTGCTCTACCTTAGAAC 660
 QY 661 CCTGAAACAAGAGGAGGACACATATACGAAATCAGCAGGTACGCGCAAGAGCAAAAGA 720
 DB 661 cctgaaacaagagagagacacatatacgaatagcaggtacgcgcaagagcaaaaga 720
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGATTCATGGAAGCCAGTGAAGATGC 780
 DB 721 atgTTCCCAAGCTCTCAGTCTGATTTCTGATTCATGGAAGCCAGTGAAGATGC 780

DB 721 atgttcccaagctctcagctgattcttgacattgcatcgtgaaagccagtgaaagatgc 780
 QY 781 ATTGAGATTTAAAGTTTGATATGGAACTGAAGGACTCTATTGATAGGGAAGAAATAGC 840
 DB 781 attgagatttaagtttgatattggaacaaactgaaggaactctattgtaggagaaataagc 840
 QY 841 AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
 DB 841 agtaattggacattctcttttgggagcaacggttatttcagactcttgtagaagatcagag 900
 QY 901 ATTGAGATGTGCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 attcagatgtgatttgccctggatgcatggatgtttccactggggtgtagaagcatattc 960
 QY 961 CAGAATTTCTCAGCCCTCTTTTATCAACTCTCAATATTTTCAATATCTCTCTCTAATAT 1020
 DB 961 cagaattctctcagccctcttttatacaactctgaattttccaataatctcgtctaata 1020
 QY 1021 CATAAAAAATGAAAAAATGCTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1021 cataaaatgaaaaaatgctactcactcactcactcactcactcactcactcactcactcact 1080
 QY 1081 TTCAGTCCACAGCAATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1081 ttcagtccacagcaatTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 1141 GCTCAATTTAAAGGGAGACATAGATTCAAAATGCAAGTATTGATCTTTAGCAACAAAGCTTC 1200
 DB 1141 gctcaatttaaaggagacatagattcaaaTGCAGTATTGATCTTTAGCAACAAAGCTTC 1200
 QY 1201 ATTGAGATTTTACAAAAGCAATTTAGGACTTTCATTAAGATTTTGTGATCAGTGGGACTGCTT 1260
 DB 1201 attgagattttacaaaagcaatTTAGGACTTTCATTAAGATTTTGTGATCAGTGGGACTGCTT 1260
 QY 1261 GATTGAAGGAGATGATGAGAAATCTTTATCCAGGAGCCCAACATTAACACAAACCAATCAACA 1320
 DB 1261 gattgaaggagatgagaaatctttatccaggagccaacatttaacacaaccaatacaaca 1320
 QY 1321 CATCATGTTTACAACTCTTCAGGAATAGAGAAATACAAAT 1361
 DB 1321 catcatgttacagaactcttcaggaaatagagaaatacaatt 1361

RESULT 2

AAAS2357

ID AAAS2357 standard; cDNA; 1361 BP.

AC AAAS2357;

XX

DT 18-SEP-2000 (first entry)

XX

DE cDNA encoding human low density lipoprotein-associated phospholipase A2.

XX

KW Human; low density lipoprotein associated phospholipase A2;

KW LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;

KW short chain phospholipid; serine-dependant phospholipase;

KW inflammation; proinflammatory; anti inflammatory; drug screening;

KW antibody; diagnosis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

CDS 38..1360

FT /*tag= a

FT /partial

FT /product= "Human LDL-PLA2"

FT /note= "No stop codon given in the specification"

XX

PN WO200024910-A1.

XX

PD 04-MAY-2000.

XX

PF 27-OCT-1999; 99WO-GB03551.

AC AAQ87947;
 XX 06-DEC-1995 (first entry)
 XX Human platelet activating factor, acetyl hydrolase (PAF-AH), cDNA.
 XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis, ss.
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 162..1487
 FT /tag= a
 FT /product= Acetyl_hydrolase.
 FT
 XX W09509921-A.
 XX
 XX 13-APR-1995.
 XX
 XX 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 XX
 XX (ICOS-) ICOS CORP.
 XX
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX
 XX WPI; 1995-155262/20.
 DR P-PSDB; AAR71913.
 XX
 XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Claim 4; Page 51-53; 88pp; English.
 XX
 XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
 CC is useful in the treatment of inflammatory diseases, in particular
 CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
 CC raising monoclonal antibodies specific for PAF-AH that are useful in
 CC the diagnosis of such diseases.
 XX
 XX Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;
 SQ

Query Match 99.9%; Score 1359.4; DB 16; Length 1520;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCGATGT 60
 DB 125 tgagagactaagctgaagctgctcagctcccaagatggtgccacccaaatcgatgt 184

QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 185 gcttttctgctctgcggtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244

QY 121 TCCGTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
 DB 245 tccgtgtgcccatatgaatcatcagcatgggtcaacaaatacaagtactgatggctgc 304

QY 181 TGCNAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
 DB 305 tgcnagctttggccaaactaaatcccggggaaatgggcttatttcggttggttgtac 364

QY 241 AGACTTAATGTTGATCACACTAATAGGCGACCTCTCTGCTTTATATTATCCATCCCA 300
 DB 365 agacttaatgttgatcacactaataaggcgacctctctgcttttattatccatccca 424

QY 301 AGATATGATCGCTTGACACCCCTTTGGATCCCAAAATAAAGAATATTTTGGGGTCTTAG 360

DB 425 agataatgatcgcttgacaccccttgatcccaataaagaataattttggggtcttag 484
 QY 361 CAAATTTCTTGGAAACACACTGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
 DB 485 caaattctctggaacacactggcttatgggcaacattttgagttactcttggttcaat 544
 QY 421 GACAACTCTTGCACAACTGGAATTTCCCTCTGAGGCTGTGTAATAATATCCACTTGTGT 480
 DB 545 gacaactcctgcaactggaattccctctgaggcctggtgaaaaataatccacttgtgt 604
 QY 481 TTTTCTCATGCTTGTGGGCATTCAGGACACTTTATTTCTGCTATTTGGCATTCACCTGGC 540
 DB 605 ttttctcatggtcttggggcattcaggacactcttctctgctatggtgacctggc 664
 QY 541 ATCTCATGCTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 600
 DB 665 atctcatgggttttatagttgctgctgtagaacacagagatagatctgcatctgcaactta 724
 QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
 DB 725 ctatttcaaggaccattctgctgcagaaataggggacaaagctcttggctctacacttagaac 784
 QY 661 CCTGAAACAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCGCAAGAGCAAAAGA 720
 DB 785 cctgaaacaaagaggagagacacataacgaaatgagcaggtacggaagagcgaagaaga 844
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATCGAAAGCCAGTGAAGAAATGC 780
 DB 845 atgtcccaagctctcagctgctgattcttgacatgcatggaagccagtggaagaatgc 904
 QY 781 ATTAGATTTAAAGTTTGAATGAACAACTGCAAGGACTCTATTGATAGGGAATAATAGC 840
 DB 905 attagatttaagtttgatggaacaaactgaaggactctattgataggggaaaaaatagc 964
 QY 841 ACTAATTTGACATTTCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATTCAGAG 900
 DB 965 agtaattggacattcttttggtagcaacggtatttcagactcttagtgaagatcagag 1024
 QY 901 ATTGAGATCTGTTATTTGCTGCTGATCGATCGATGTTTCCACTGGGTGATGAAGTATATTC 960
 DB 1025 atctcagatggtgattgctgctggtgatggtgttccactggtggtgatgaagtatttc 1084
 QY 961 CAGAATTTCTCAGCCCTCTCTTTTATCAACTCTGAATATTTCCTCAATATCTCTGAATAT 1020
 DB 1085 cagaattctcagccctctctttttatcaactctgaatttcccaatctcctgctcaatat 1144
 QY 1021 CATAAAATGAANAATGCTACTCAGCTGATAAAGAAAGATGATTACAATCAGGGG 1080
 DB 1145 cataaaaatgaanaaatgctactcactcactgataaagaagaagatgattacaatcagggg 1204
 QY 1081 TTCAGTCCACCAGAAATTTTGGCTGACTTCACTTTTGGCAACTGGCAAAATTAATTTGACACAT 1140
 DB 1205 ttcagtccaccagaaattttggctgactctccttctgcaacttggcaaaaataattggaacat 1264
 QY 1141 GCTCAAAATTAAGGAGACATAGATTCAATGCAGCTATTGATCTTTAGCAACAAGGCTTC 1200
 DB 1265 gctcaaatgaaggagagacatagattcaaatgtagctattgattccttagcaacaagcttc 1324
 QY 1201 ATTACCATCTTACAAAACCATTTTAGGACTTCTAAGATTTTGGATCTCAGTGGGACTGCTT 1260
 DB 1325 attagcatctctacaaaagcatttaggactctataaagattttgatcagtgaggactgctt 1384
 QY 1261 GATTGAAGGAGATGATGAATCTTATTCAGGGGACCAACATTAACACCAACCAATCAACA 1320
 DB 1385 gattgaaggagatgatgagaactcttattccagggaacacacattcaacacacacacaa 1444
 QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAT 1361
 DB 1445 catcatgttacagaactcttccagggaatagagaaatacaatt 1485

The present sequence encodes the purified and isolated human plasma platelet activating factor acetylhydrolase (PAF-AH). This novel polypeptide inactivates PAF and oxidatively fragmented phospholipids such as pro-inflammatory arachidonic acid metabolites, and so can be used to treat inflammation by augmenting endogenous activity. Typical applications are in asthma, anaphylaxis, shock, reperfusion injury, central nervous system shock, arthritis, Crohn's disease, systemic lupus erythematosus, adult respiratory distress syndrome. The polypeptide can also be used to raise specific antibodies (Ab) which are useful as immunoassay reagents and for generating anti-idiotypic

QY	1	TGAGAGACTAAGCTGAACCTGCTGTCTCAGCTCCCAAGATGGTGCCACCACAAATTGCATGT	60
Db	125	tgaagactaaagtgaacctgctcagctcccaagatggtgccaccaaatlgcatgt	184
QY	61	GCTTTTCGCCCTCGGGCTGCTGGCTGTGGTTTTATCCTTTTWTGACTGGCAATACATAAA	120
Db	185	gcttcttcgcctctcgctggctggctggcttggtttatctcttfgacitgccaatacaaaa	244
QY	121	TCCTGTGGCCCATATGAATCATCAGCATGGGTCAAACAANAATCAAGTACTGATGGCTGC	180
Db	245	tccgtgtgcccatatgaaatcatcagcatgggtcaaacaatacaagtagctgatggctgc	304
QY	181	TGCAAGCTTTGGCCAACTAAANTCCCCGGGGAAATGGCCCTTATTCGGTTGGTWTGTAC	240
Db	305	tgsaagcttgyccaaactaaataccccggggaaatgggaccttatctcgttggttgtac	364
QY	241	AGACTTAATGTTTGATCACACTAATAAAGGCGACCTCTTTGCGTTTATATTATCCATCCCA	300
Db	365	agacttaagtgttgatcacactaaataagggaacctctctgctttattattatccatccca	424
QY	301	AGATAATGATCGCTTGACACGCTTTGGATCCCAATAAAGAATATTTTTGGGGTCTTTAG	360
Db	425	agaataatgatcgcttgacaccttgtagccccaataaagaatatctttggggctcttag	484
QY	361	CAAAATTTCTTGGAACACACTGGCTTATGGGCAACATTTTGAAGTTACTCTTTGGTTCAAT	420
Db	485	caaatctcttggaacacactggcttatgggcaacattttgaaggttaactcttggttcaat	544
QY	421	GACAACTCTGCCAACTGGAAATCCCCTCTGAGGGCTGTGAAAAATATCCACTGTGTGT	480
Db	545	gacaaactcctgcaaacctggaaatcccctctggaggctggtgaaaaatatccacttgtgt	604
QY	481	TTTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTTGGCAATTCACCTGGC	540
Db	605	tttttctcatggctttggggcatttcaggacacctttattctgtattggcattggacctggc	664
QY	541	ATCTCATGGGTTTATAGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Db	665	atctcatagggtttatagtgtgctgttagaacacagagatagatctgcatctgcaactta	724
QY	601	CTATTCCAAGSACCAACTGCTGCAGAAATAGGGGACACAGTCTTGCTCTACCTTAGAAC	660
Db	725	cctaattcaaggaccaaactcgtctgcagaaataggggacaagctcttggtctacacttagaac	784
QY	661	CCTCAAAACAAGAGAGAGACACATATACGAANTGACGAGGTACGGCAAAAGACAAAAGA	720
Db	785	ccfgaacaagaagagagagacacataacgaaatgagcaggcacggcaaaagcaaaaaga	844
QY	721	ATGTTCCCAAGCTCTAGTCTGATTCTTGACATTTGACATCATGGAAGCCCACTGAAGAAATGC	780
Db	845	atgtctcccaagctctcagctcgtgatatcttgcacatgcatgcatggaagccagtgaaagatgc	904
QY	781	ATTAGATTTTAAAGTTTGATATGTGAACAACACTGAAGGACTCTATTGTATAGGGAATAATAGC	840
Db	905	attagatttaaagtttgatatggaaacaactgaaggactctattgatagggaataaatagc	964
QY	841	AGTAATTTGGACATTTCTTTTGGTGAGCAACGGTTTATTCAGACTCTTTAGTGAAGATCAGAG	900
Db	965	agtaattggacattctcttgggtggacaacgggttatccagactcttagtgaagatcagag	1024

QY 481 TTTTCTCATGCTGCTGGGCAATTCAGACACATTTATTTCTGCTATTTGGCATTTGACCTGGC 540
 DB 605 tttttcattggtcttggtggtcattcagacattttatttctgctattggtcattgacctggc 664
 QY 541 ATCTATGGGTTTATAGTTGCTGCTAGAACACAGAGATGATCTGCAATTTA 600
 DB 665 atctatgggtttatagttgctgctgtagaacacagagatgctgcatctgcaactta 724
 QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGACAAAGTCTTGGCTCTACCTTTAGAAC 660
 DB 725 ctatttcaaggaccactctgctgagaaatagggacaaagcttggctctaccttagaac 784
 QY 661 CCTGAACACAGAGGAGAGACACATATACGAAATGAGCAGTACGGCAAGACGCAAAAGA 720
 DB 785 cctgaacacagagagagagacacataacgaatagcagtagcagcagcaagagcaaaaga 844
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGATGATGAAAGCCAGTGAAGAAATGC 780
 DB 845 atgttcccaagctctcagctgattcttgacattgacatggaagccagtgaaagatgc 904
 QY 781 ATTAGATTTAAAGTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAATAATAGC 840
 DB 905 attgatttcaagtttgatacggaaactgaagactctcttgatagggaaataatagc 964
 QY 841 AGTAATGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
 DB 965 agtaattggacattcttttgggtgagcaacggttattcagactcttagtgaagatcagag 1024
 QY 901 ATTGATGTTGGTATGTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTC 960
 DB 1025 attcagatgtggtattgcttggatgcatggtgttccactgggtgatgaagatatttc 1084
 QY 961 CAGAAATCTCAGGCGCCCTTTTATCAACTCTCAATATTTCCAAATATCTCTGCTAAATAT 1020
 DB 1085 cagaattcctcagccctctctttttatcaactcttcttcaactctgaaatctcctgctaatat 1144
 QY 1021 CATAAAAATGAATAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1080
 DB 1145 cataaaaatgaaaaatgctactcactgataaaagaaagaaagatgattacaatcagggg 1204
 QY 1081 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTCCAACTGGCAAAATTAATGGACACAT 1140
 DB 1205 ttcagtcacacagaattttgctgacttcaacttttgcacttgcacttgcacttgcacttgc 1264
 QY 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCACTATTTGATCTTAGCAACAAAGCTTC 1200
 DB 1265 gctcaaatgaaggagagacatagattcaaatgtagctattgatttagcaacaaagcttc 1324
 QY 1201 ATTAGCATCTTTACAAAAGCATTTAGGACTTTCATTAAGATTTTGTATGATGAGTGGCTTT 1260
 DB 1325 attagcattcttacaagaagcatttaggacttcaagaatttttgcagtgaggactgctt 1384
 QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACAAACCAATCAACA 1320
 DB 1385 gattgaaggagatgatgagaatcttattccaggggaccacataacacacacacacacaa 1444
 QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
 DB 1445 catcatgttacagaactcttcaggaaatagagaaatacaatt 1485

RESULT 8
 ID AAV08534 standard; cDNA; 1520 BP.
 XX AAV08534;
 AC AAV08534;
 XX
 DT 12-FEB-1999 (first entry)
 XX
 DE Human PAF-AH coding sequence.
 XX
 XX Platelet-activating factor acetylhydrolase; PAF-AH; human; antibody; ss.
 XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 PH CDS 162..1487
 FT /*tag= a
 XX
 PN US847088-A.
 XX
 PD 08-DEC-1998.
 XX
 PF 07-JUN-1995; 95US-0485938.
 XX
 PR 07-JUN-1995; 95US-0485938.
 PR 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0318905.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Cousens LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
 PI Wilder CL;
 XX
 DR WPI; 1999-059148/05.
 DR P-PSDB; AAW73359.
 XX
 PT Antibodies specific for platelet-activating factor acetylhydrolase
 PT proteins - useful for detecting or purifying the proteins
 XX
 PS Disclosure; Column 45-48; 59pp; English.
 XX
 CC This sequence encodes the human platelet-activating factor
 CC acetylhydrolase (PAF-AH). The encoded protein is specifically bound by
 CC the antibody of the invention. The monoclonal antibody of the invention
 CC is useful for detecting or purifying PAF-AH proteins.
 XX
 SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 20; Length 1520;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGAGACAGTAAGCTGAACACTGCTGCTCAGCTGCCAAGATGGTGCACCCAAATTTGCATGT 60
 DB 125 tggagactaagctgaaactgctgctcagctcccaagatgggtgccaccacaaatgcatgt 184
 QY 61 GCATTTCCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 185 gcttttctgctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244
 QY 121 TCCTGTTGCCCATATGAATATCATCAGATGGTCAACAAATACAAATGATGATGCTGCTGCT 180
 DB 245 tctgttgcccatatgaaatcatcagatgggtcaacaaatacaagactgactgctgctgctgct 304
 QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 240
 DB 305 tgaagcttttggccaaactaaaaacccccgggggaaatgggcttattcctgctgctgctgct 364
 QY 241 AGACTTAATGTTGATCACACTTAATAAGGCGACCTCTCTGCGTGTATATATATCAATCCCA 300
 DB 365 agacttaagtgtgatcacactaataaaggcacccttctgctgctgctgctgctgctgctgct 424
 QY 301 AGATAATGATGCTGCTGACACCTTTGATCCCAATAAATAAATAATTTTGGGCTCTTAG 360
 DB 425 agataatgatgctgctgacaccccttggatcccaataaagaataatttttgggctcttag 484
 QY 361 CAAATTTCTTGGAAACACACTGCTGCTTATGGGCAACATTTTGGAGTTTACTCTTTGCTTCAAT 420
 DB 485 caaattcttggaaacacactgctgcttgggcaacatttggaggttactcttctgctgctgct 544
 QY 421 GACAACCTCTGCAAACTGGAATTCCTCTGAGCGCTGCTGAGAAATAATCACTTTGCTGT 480
 DB 545 gacaactcctgcaaacctggaattccctctgagcctggtgaaaaataatccactctgctgct 604

QY 481 TTTTCTCATGCTTGGGCGATTCAGACACACTTATTGCTGCTATTGCGATTCACCTGCG 540
Db 605 tttttctcatggtcttggtggcattcagacacactttatttctgctattgctgacattgac 664
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 acctcatgggtttatagttgctgtgtagacacagagatagatctgcatctgcaactta 724
QY 601 CTATTTCAGGACCAATCTGCTCAGAAATAGGGGCAAGCTTTGGCTCTACCTTAGAAC 660
Db 725 ctatttcaaggaccaatctgctgcagaaataggggcaagcttctgctcctacccttagac 784
QY 661 CTGAAACAGAGGAGGAGACACATATACGAAATGACGAGTACGGCAAGAGCAAAAGA 720
Db 785 cctgaacaagagagagagacacataacgaaatgagcaggtacgccaagagcaaaaga 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTCATGATGGAAGCCAGTGAAGATGC 780
Db 845 alytcccccaagctcagctgctgtattcttgacattgcatcgtggaagcagtgaaagatgc 904
QY 781 ATTAGATTTAAAGTTTGATATGATGAACCACTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 905 attagatttaagtttgatagaaacactgaaggactctattgtagaggaataatagc 964
QY 841 AGTAATTGACATCTCTTTGGTGGGACACGCTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
Db 965 agtaattggacattcttttgggtggagcaacggttattcagactcttagtgaagatcag 1024
QY 901 ATTGAGATGCTGATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 1025 attcagatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1084
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCGAATATCTGCTAATAT 1020
Db 1085 cagaattcctcagccctctttttataactctgaattatttccaatatctcgtcctaat 1144
QY 1021 CATAAATGAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAATCAGGGG 1080
Db 1145 cataaaatgaaaaatgctactcactgataaaagaaagaaatgattacatcagggg 1204
QY 1081 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTGAAGTGGCAAAATATTGACACAT 1140
Db 1205 ttcagtcacacagaaatttctgctcactcttctgcaactggtgcaataattggacacat 1264
QY 1141 GCTCAAAATTAAGGAGACATAGATCAAAATGACGATTTTATGATCTTAGCAACAAAGCTC 1200
Db 1265 gctcaaatgaaaggagacatagattcaaatgactgattgactttagcaacaaagcttc 1324
QY 1201 ATTAGCATCTTACAAAAGCATTTAGGACTTCAATAAGATTTTGTGATGAGTGGACTGCTT 1260
Db 1325 attagcattcttacaagaagcatttaggacttcataaagattttgacagtgaggactgctt 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTTATTCAGGAGCAACATTAACACACCAATCAACA 1320
Db 1385 gatigaaggagatgagaaatcttattccaggaggacacataacacacacacacacac 1444
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 catcatgttacagaactcttcaggaaatagagaatacaatt 1485

RESULT 9

AAAS9579
ID AAAS9579 standard; cdna; 1520 BP.XX
AC
XX
AAAS9579;

14-NOV-2000 (first entry)

cDNA encoding plasma platelet-activating factor acetylhydrolase.

XX
DE
XX
Platelet-activating factor acetylhydrolase; platelet-activating factor;
KW reperfusion injury; acute inflammation; pleurisy; asthma;

XX
OS
XX
FH
FT
FT
FT
XX
PN
XX
XX
PD
XX
PF
XX
PR
PR
PR
PR
XX
PA
XX
PI
XX
DR
DR
XX
PT
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
SQ

necrotising enterocolitis; adult respiratory distress syndrome; ss.
Homo sapiens.
Location/Qualifiers
162..1487
/*tag= a
/product= "platelet-activating factor acetylhydrolase"

US6099836-A.

08-AUG-2000.

19-JUN-1998; 98US-0100546.

07-JUN-1995; 95US-0480658.

22-JAN-1998; 98US-0010715.

06-OCT-1993; 93US-0133803.

06-OCT-1994; 94US-0318905.

(ICOS-) ICOS CORP.

Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;
Cousens LS;

WPI; 2000-531654/48.

P-PSDB; AAB07774.

Treating mammal susceptible to or suffering from platelet-activating factor mediated condition associated with reperfusion injury such as acute inflammation, pleurisy, asthma, necrotising enterocolitis -
Example 3; Column 45-48; 55pp; English.
The specification describes a pharmaceutical composition comprising platelet-activating factor acetylhydrolase. The composition is administered for treating a mammal susceptible to or suffering from a platelet-activating factor-mediated condition associated with reperfusion injury. Diseases and conditions which may be treated include acute inflammation, pleurisy, asthma, necrotising enterocolitis and adult respiratory distress syndrome. The present sequence encodes human plasma platelet-activating factor acetylhydrolase.

Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 21; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCAGAGACTAAGCTGAAGCTGCTGCTCAGCTCCCAAGATGTCGCCACCAATTCATGCT 60
Db 125 tgagagactaagctgaagctgctgctcagctcccaagatggtgccacccaattgcatgt 184
QY 61 GCTTTTCGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 gctttctgctctcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244
QY 121 TCCGTGTCCTCATATGAATCATCAGCATGGGTCAACAAATACAGTACTGATGGCTGC 180
Db 245 tccgtgtcccatatgaatcatcagcatgggtcaacaaatacaagtaactgaaggctgc 304
QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGCCCTATTTCGCTGGCTGTAC 240
Db 305 tgcagctttggccaaactaaatcccccggggaaatggcccttattccctggctgtgac 364
QY 241 AGACTTAATGTTGATCAGTAAAGGCGACCTTCTTCGCTTATATATTCATCCATCCCA 300
Db 365 agacttaattgtgatcacactaaagggcactctctgctgttatattatccatccca 424
QY 301 AGATAATCATCCCTTGACACCTTTGGATCCCAATAAAGATAATTTTTGGGGCTCTAG 360
Db 425 agataatgatcgccttgacaccccttggatcccaataaagaatatttttggggctctag 484

QY 361 CAAATTTCTTGGACACACTGGCTTATATGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
DB 485 caaattcttggacacactggcttattatggcaacatTTTgaggttactcttggttcaat 544
QY 421 GACAACCTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATCCACTTTGTGT 480
DB 545 gacaactctcgaaactggaattccctctcgagccctggTgaaataatccacttgtgt 604
QY 481 TTTTCTCATGCTTGGCTTGGGCAATTCAGACACTTTATTTCTGCTATTTGGCATTTGACCTGGC 540
DB 605 ttttctcatggtcttggcttgggcaattcagacactttattctgctattggcattggcctggc 664
QY 541 ATCTCATGGGTTTATAGTCTGCTGTAGAACACAGAGATAGATCTGCTATCTGCAACTTA 600
DB 665 atctcatgggtttatagttctgctgtgtagaacacagagatagatctgctatctgcaactta 724
QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGACAACTCTTGGCTCTACCTTTAGAAC 660
DB 725 ctatttcaaggaccaatctgctgagaaatagggacaaactcttggctctaccccttagaac 784
QY 661 CCTGAACACAGAGAGAGACACATATACGAATTCAGGAGGTACGGCAAGACGCAAAAGA 720
DB 785 cctgaacaagagagagacacatacacgaatgagcaggtacggcaagagcaaaaga 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTCATGAAAGCCAGTGAAGAAATGC 780
DB 845 atgttcccaagctctcagctctgattcttgacattgatcatatggaagccagtgaaagaatgc 904
QY 781 ATTAGATTTAAAGTTTATATGGAACAACTGAAGGACTCTATTGTATAGGGAATAATAGC 840
DB 905 attagatttaaagtttattatggaacaaactgaagactctattgtatagggaataatagc 964
QY 841 AGTAATGGACATCTTTTGGTGGAGCAACGGTTTATTCAGACTCTTACTGAAGATCAGAG 900
DB 965 agtaattggacattcttcttggtagagcaacggttattcagactcttattggaagatcagag 1024
QY 901 ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
DB 1025 attcagatgtggtattgccctggatgcattggtatttccactgggtgattggaagtatttc 1084
QY 961 CAGAAATCCTCAGGCCCTCTTTTATCACTCTGAATATTTTCAATATCTCTGCTTAATAT 1020
DB 1085 cagaattcctcagccctctttttatcaactctgaattttcccaatactctgctaata 1144
QY 1021 CATAAATGAAAATGCTACTCCTACCTCATAAAGAAAGAGATGATTACAAATCAGGGG 1080
DB 1145 cataaaatgaaaatgctactccctcgataaaagaaagagatgattcacatcagggg 1204
QY 1081 TTCAGTCCACAGAAATTTGCTGACTTTCACCTTTTGCACCTGGCAAAATTAATTGGACACAT 1140
DB 1205 ttcagtccaccagaattttgctgacttcaacttttgcaactggcaaaataattggacacat 1264
QY 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCGGTTATGATCTTAGCAACAAAGCTTC 1200
DB 1265 gctcaaatgaaaggagacatagattcgaattgattgatttcttagcaacaaagcttc 1324
QY 1201 ATTACATCTTTACAAAACATTTTAGGACTTCATAAAGATTTTGTAGTGGGACTGCTT 1260
DB 1325 attagcatcttcacaaaacattttaggacttcataaagattttgacagtgaggactgctt 1384
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTAAACACAAACCAATCAACA 1320
DB 1385 gattgaaggagatgagagaacttatttccagggaaccatttaacacaaaccaatcaaca 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATACAGAAATCAAT 1361
DB 1445 catcatgttacagaactcttcagggaatagagaatacaatt 1485

RESULT 10

AAA10861

ID AAA10861 standard; cDNA; 1520 BP.

XX AAA10861;
AC 14-JUL-2000 (first entry)
DT Human platelet-activating factor acetyl hydrolase nucleotide sequence.
XX Platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;
XX inflammatory response; pre-term labour; pharmaceutical composition;
KW regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease; ss;
KW pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
PH 162..1487
FT /*tag= a
FT /product= PAF_AH
FT /note= "Platelet-activating factor acetyl hydrolase"
XX
XX US6045794-A.
PN 04-APR-2000.
PD
XX 09-JUN-1999; 99US-0328474.
XX 12-AUG-1997; 97US-0910041.
PR 06-OCT-1993; 93US-0133803.
PR 06-OCT-1994; 94US-0318905.
PR 07-JUN-1995; 95US-0483232.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
PI Eberhardt CD;
XX WPI: 2000-282671/24.
DR P-PSDB; AAY88301.
XX Treatment of mammals suffering from pre-term labour comprises
PT administering a pharmaceutical composition comprising
PT platelet-activating factor acetyl hydrolase enzyme -
XX Claim 1; Column 63-68; 67pp; English.
XX This sequence represents a nucleotide sequence encoding the human
CC platelet-activating factor acetyl hydrolase (PAF-AH). PAF is a
CC phospholipid and is implicated in pathological inflammatory responses
CC (e.g. asthma, anaphylaxis, septic shock and arthritis). PAF-AH is
CC released by hepatocytes, and macrophages and inactivates PAF. PAF-AH also
CC inactivates oxidatively fragmented phospholipids that mediate
CC inflammation. This sequence is specifically claimed for use in a method
CC to treat a mammal suffering from pre-term labour. PAF-AH is included in a
CC pharmaceutical composition which can be administered to a mammal
CC suffering from pre-term labour. The invention relates to purified and
CC isolated polynucleotide sequences encoding human PAF-AH and materials and
CC methods for the recombinant production of PAF-AH products which are
CC expected to be useful in regulating inflammatory events. The
CC administration of PAF-AH to animals may be used for ameliorating
CC pathological inflammatory conditions such as asthma, anaphylaxis, shock,
CC arthritis, Crohn's disease, pancreatitis, allergic inflammation, and
CC human immunodeficiency virus (HIV).
XX Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.98; Score 1359.4; DB 21; Length 1520;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCAATTCATGT 60
DB 125 tgagagagactaagctgaaactgctcagctcccaagatggtggccacccaatttcagt 184

QY	1141	GCTCAAAATTAAAGGGAGACATAGATTCAAAATGCACGCTATTGATCTTAGCACAAAGACTTC	1200
Db	1265	gctcaaatcaaggagacatagattcaaatgtagctattgatcttagcaagaagcttc	1324
QY	1201	ATTAGCATCTTACAAAGACATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTTGCCTT	1260
Db	1325	attagcatcttcaagaagcatttaggacttcataaagattttgatcagttggactgctt	1384
QY	1261	GATTGAAGGAGATGATCAGAAATCTTATTCACGGGACCACCAATTAACACCAACCAATCAACA	1320
Db	1385	gattgaaggagatgataagaattcttccaggaccacaatttaacacacccaatacaaca	1444
QY	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAATT	1361
Db	1445	catcatgttacagaactctctcaggaaatagagaaaatacaatt	1485

AAZ24240	AAZ24240 standard; cDNA; 1520 BP.
ID	XX
XX	AAZ24240;
AC	XX
XX	08-FEB-2000 (first entry)
DT	XX
XX	Human PAF-AH cDNA.
DE	platelet activating factor acetylhydrolase; PAF-AH; human; treatment;
XX	antiinflammatory; antiasthmatic; antiallergic; antiarthritic; aschma;
KW	antiischemic; inflammatory disorder; anaphylaxis; ulcerative colitis;
KW	antigen-induced arthritis; ischemia; septicemia; allergy; ss.

AAZ24240; AC

DT 08-FEB-2000 (first entry)

Human PAF-AH cDNA

XX
XX
XX

KW antiinflammatory; antiasthmatic; antiallergic; anti-
antiischemic; inflammatory disorder; anaphylaxis; ul-
KW antigen-induced arthritis; ischemia; septicemia; all-

OS Homo sapiens.

.....	Key	Location/Qualifiers
FH	CDS	162..1487
FT		

```

FT      /"Lay" d
FT      /product= "PAF-AH"

```

XX
PN
US5977308-A

XX
PD 02-NOV-1999

XX
10-100 1002
0000 0000 0000

[illegible]

PR 06-OCT-1994; 94US-0318905.

XX
XXXXX
XXXXX

XX
1003 / 1003 CONF.;

Cousens LS, Gray P, Tröng HL, Tjoelker LW, Wilder PI
Eberhardt CN.

XX
XX
LBT. 2000-031056 '03

DR P-PSDB; AAY50735.

Truncated and substituted versions of human platelet

PT as asthma -

PS Claim 9a; Column 59-64; 65pp; English.

This invention describes novel truncated and variant

PAF-AH (platelet activating factor acetylhydrolase)

antileukemic activity. (I) are used to treat a wide

arthritis, ulcerative colitis, ischemia, septicemia,

CC at the termini than the full-length protein. Some of

sequence encodes the human PAF-AH protein which is d

1

PI Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 XX Wilder CL;
 DR WPI; 2001-280610/29.
 DR P-PSDE; AAE00761.
 XX
 XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF -
 XX
 XX Claim 1: Column 43-48; 54pp; English.
 XX
 CC The present cDNA sequence encodes human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) protein.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 22; Length 1520;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGCTGCCACCAATTCGATGT 60
 DB 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGCTGCCACCAATTCGATGT 184
 QY 61 GCTTTTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 185 GCTTTTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
 QY 121 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 245 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
 QY 181 TCGAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCTGCT 240
 DB 305 TCGAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCTGCT 364
 QY 241 AGACTTAATGTTGATCACACTAATAAGGCGACCTTCTTTCGCTTATATATATATATATATATAT 300
 DB 365 AGACTTAATGTTGATCACACTAATAAGGCGACCTTCTTTCGCTTATATATATATATATATATAT 424
 QY 301 AGATAATGATCGCTTGACACCTTTTGGATCCCAATTAAGAATATATTTTGGGCTCTTAG 360
 DB 425 AGATAATGATCGCTTGACACCTTTTGGATCCCAATTAAGAATATATTTTGGGCTCTTAG 484
 QY 361 CAATTTCTTGGACACACTGCTTATGGGCAACATTTTGGGCTTATATATATATATATATATATAT 420
 DB 485 CAATTTCTTGGACACACTGCTTATGGGCAACATTTTGGGCTTATATATATATATATATATATAT 544
 QY 421 GACAACTCCTCAACTGGAATTCCTGCTGAGGCTGCTGGAATAATATATATATATATATATATAT 480
 DB 545 GACAACTCCTCAACTGGAATTCCTGCTGAGGCTGCTGGAATAATATATATATATATATATATAT 604
 QY 481 TTTTCTCATGCTTGTGGGCACTTTCAGGACACTTATTCGCTATTTGCTATTTGCTATTTGCTATTT 540
 DB 605 TTTTCTCATGCTTGTGGGCACTTTCAGGACACTTATTCGCTATTTGCTATTTGCTATTTGCTATTT 664

QY 541 ATCTCATGGCTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
 DB 665 ATCTCATGGCTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
 QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGCAAGCTCTTGGCTCTACCTTTAGAAC 660
 DB 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGCAAGCTCTTGGCTCTACCTTTAGAAC 784
 QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
 DB 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 844
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTTCACATTTGATGGAAGGCAAGGAGGAGGAGGAG 780
 DB 845 ATGTTCCCAAGCTCTCAGTCTGATTTTTCACATTTGATGGAAGGCAAGGAGGAGGAGGAG 904
 QY 781 ATTAGATTTAAAGTTTGTATGGAACAACACTGAAGGACTCTATTGATGAGGAAAAAATAGC 840
 DB 905 ATTAGATTTAAAGTTTGTATGGAACAACACTGAAGGACTCTATTGATGAGGAAAAAATAGC 964
 QY 841 AGTAATTTGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
 DB 965 AGTAATTTGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 1024
 QY 901 ATTCAGATGTGCTATTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 1025 ATTCAGATGTGCTATTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
 QY 961 CAGAAATCTCTCAGGCGCTCTTTTATCAACTCTCTGAATATTTTCAATATCTCTGCTAATAT 1020
 DB 1085 CAGAAATCTCTCAGGCGCTCTTTTATCAACTCTCTGAATATTTTCAATATCTCTGCTAATAT 1144
 QY 1021 CATTAATAATGAAAAATGCTACTCACCTGATTAAGAAAGAGATGATTACAAATCAGGGG 1080
 DB 1145 CATTAATAATGAAAAATGCTACTCACCTGATTAAGAAAGAGATGATTACAAATCAGGGG 1204
 QY 1081 TTCAGTCCACAGCAATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1205 TTCAGTCCACAGCAATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
 QY 1141 GCTTCAATTTAAAGGAGACATAGATTCAATTTGAGCTATTGATCTTTAGCAACAAAGCTTC 1200
 DB 1265 GCTTCAATTTAAAGGAGACATAGATTCAATTTGAGCTATTGATCTTTAGCAACAAAGCTTC 1324
 QY 1201 ATTAGCATCTTTCACAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
 DB 1325 ATTAGCATCTTTCACAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
 QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTTCAGGGACCAACATTTAACACAAACCAATCAACA 1320
 DB 1385 GATTGAAGGAGATGATGAGAAATCTTATTTCAGGGACCAACATTTAACACAAACCAATCAACA 1444
 QY 1321 CATCATGTTACAAACTCTTCAGGAATAGAGAAATACAAATTT 1361
 DB 1445 CATCATGTTACAAACTCTTCAGGAATAGAGAAATACAAATTT 1485

RESULT 13
 AAC89057

ID AAC89057 standard; cDNA; 1520 BP.

XX AAC89057;

AC AAC89057;

XX 06-MAR-2001 (first entry)

XX Platelet-activating factor acetylhydrolase coding sequence.

XX PAF-AH; antiallergic; antiinflammatory; platelet-activating factor;

XX PAF-acetylhydrolase; enzyme; pleurisy; asthma; rhinitis; human;

XX necrotizing enterocolitis; acute respiratory distress syndrome; ss.

OS Homo sapiens.

XX

US6146625-A.
 14-NOV-2000.
 22-JAN-1998; 98US-0010715.
 07-JUN-1995; 95US-0480658.
 08-OCT-1993; 93US-0133803.
 06-OCT-1994; 94US-0318905.
 (ICOS-) ICOS CORP.
 Gray P, Trong HL, Tjoelker LW, Wilder CL, Eberhardt CD;
 Cousins LS;
 WPI; 2001-040421/05.
 P-PSDB; AAB49451.
 Treating platelet-activating factor mediated pathologies such as
 asthma, rhinitis, pleurisy and acute respiratory distress syndrome
 comprising administering platelet-activating factor acetylhydrolase
 enzyme
 Claim 1; Column 45-48; 54pp; English.
 The present invention relates to a method for treating a mammal
 susceptible to or suffering from a platelet-activating factor
 (PAF)-mediated pathological condition, comprising administering a
 composition comprising PAF acetylhydrolase (PAF-AH) enzyme to
 supplement endogenous PAF-AH activity and to inactivate pathological
 amounts of PAF in the mammal. PAF-mediated pathological conditions
 are conditions such as pleurisy, asthma, rhinitis, neurotizing
 enterocolitis and acute respiratory distress syndrome in mammals.
 The present sequence is the coding sequence for human PAF-AH.
 Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 other;

Query Match 99.9%; Score 1359.4; DB 22; Length 1520;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCACCAATTTGATGT 60
 125 tgaagactaagctgaactgctgctcagctcccaagatggtccaccacaaattgcatgt 184
 61 GCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 185 gcttttctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 244
 121 TCCTGTTGCCATPATCAATCATCAGATGGGTCAACAAATACAAATACAAATACAAATACAAAT 180
 245 tctctgtgcccataatgaatcatcagatgggtcaacaaatacaagactgactgctgctgctgct 304
 181 TGCAGCTTTGGCCAACTAAATATCCCGGGGAAATGGGCCCTTATTCCTGCTGCTGCTGCTGCT 240
 305 tgaagcttttggccaaactaaaatcccccggggaaatgggcttatccgttgggtgtac 364
 241 AGACTTAATGTTGATCAGACTAATTAAGGCACCTCTTCTGCTGCTTATATATATATATATAT 300
 365 agacttaatggttgaacactaatgaagggcactcttctgcttctgcttctgcttctgcttctgct 424
 301 AGATAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 425 agataatgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 484
 361 CAATTTCTTGGACACACTGGCTTATGGGCAACATTTTGGAGGTACTCTTTGGTGTCAAT 420
 485 caatttcttggacacactggcttatgggcaacattttgaggttactcttcttgggttcaat 544
 421 GACAACTCTCGAACTGGAATTCCTCTGAGCGCTGGTGAATAATATATATATATATATATATAT 480
 545 gacaaactctcgaaactggaaattccctctctgagggccttgggaaataatccactgtgtgt 604

Oy 481 TTTTCTCATGCTGCTGGGCAATTCAGGACACTTTATTCGCTATTTGGCATTTGACCTGGC 540
 Db 605 ttttctcatgctgctgggcaattcaggacactttattctgctatttggcatgacctggc 664
 Oy 541 ATCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 665 atctcatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 724
 Oy 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
 Db 725 ctatttcaaggaccac 784
 Oy 661 CCTGAACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 Db 785 cctgaacaag 844
 Oy 721 ATGTTCCCAAGCTCTCAGTCTGATTTGATTCATGATGATGATGATGATGATGATGATGATG 780
 Db 845 atgttcccaagctctcagctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 904
 Oy 781 ATTAGATTTAAAGTTTCAATGCAACAACTGAAGGACTCTTATGATAGGGAAGGAAATAGC 840
 Db 905 attagatttaagtttgatgatagaacacacacacacacacacacacacacacacacacacac 964
 Oy 841 AGTAATTTGAGACATCTTTTGGTGGGCAACGGTTTATTCAGACTCTTATGAGATCAGAG 900
 Db 965 agtaattggacattcttttgggagcaacggttattcagactctttagtaagatcagag 1024
 Oy 901 ATTCAAGTGTGTTATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 1025 attcagatggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1084
 Oy 961 CAGAATTTCTCAGCCCCCTTTTATCAACTCTGAAATTTTCAATATCTGCTGCTGCTGCTGCT 1020
 Db 1085 cagaattctcagccccctttttatcaactctgaaatatttccaatatctcgtgctaatat 1144
 Oy 1021 CATATAAATGAAATAATGCTACTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1145 cataaaatgaaataatgctactcactcactgataaagaagaagaagaagaagaagaagaaga 1204
 Oy 1081 TTGAGTCCACAGAAATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 1205 ttcagtcacacagaaatttgcctgactcactcttgcacactgcaaaataattggacacat 1264
 Oy 1141 GCTCAAAATTAAGGGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Db 1265 gctcaaatgaaaggaggagacatagattcgaatgtagctattgcttagcaacaagaagcttc 1324
 Oy 1201 ATTAGCATTTCTTACAAAGCATTTAGGACTTTCATTAAGATTTTATGATCAGTGGGACTGCTT 1260
 Db 1325 attagcattcttcaaaagcatttaggacttcaataaagaatttgcagctgggactgctt 1384
 Oy 1261 GATTGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 Db 1385 gatgagaggagatgagaaatcttattccagggggacacacacacacacacacacacacacac 1444
 Oy 1321 CATCATGTTACAGAACTCTTTCAGGGAATGAGAAATACAAAT 1361
 Db 1445 catcatgttacaagaactcttcagggaatagagaatacaatt 1485

RESULT 14
 AAT63701
 ID AAT63701 standard; cDNA; 1520 BP.
 XX
 AC AAT63701;
 XX
 DT 12-JUN-1997 (first entry)
 XX cDNA encoding platelet-activating factor acetylhydrolase.
 DE Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
 XX
 KW

KW mutation; V279F; substitution; restriction fragment length polymorphism;
 KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
 KW asthmatic children; treat; inflammatory condition; PCR; primer; ss.
 XX Homo sapiens.

PH Key Location/Qualifiers
 FT CDS 162..1487
 FT sig_peptide /*tag= a
 FT /*tag= b
 FT /*note= "long signal sequence or signal sequence plus
 FT additional peptide that is cleaved to yield
 FT mature functional enzyme"
 FT mat_peptide 285..1484
 FT /*tag= c
 FT /*note= "mature protein"

US5605801-A.
 25-FEB-1997.
 06-OCT-1993; 930S-0133803.
 06-OCT-1994; 940S-0318905.
 06-OCT-1993; 930S-0133803.
 07-JUN-1995; 950S-0478465.
 XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
 PI Wilder CL;

DR WPI: 1997-153573/14.
 DR P-PSDB; AAW09808.

PT Detection of platelet-activating factor acetylhydrolase gene
 PT mutation - by restriction length polymorphism analysis

XX Example 3; Column 33-38; 43pp; English.

XX This cDNA encodes the human platelet-activating factor acetylhydrolase
 CC (PAF-AH) (AAW09808).
 CC The claimed method of the invention detects a mutation (which results
 CC in a V279F substitution) in the PAF-AH gene, and comprises performing a
 CC restriction fragment length polymorphism analysis and differentiating
 CC between wild-type and mutant alleles on the basis of the number of
 CC restriction sites. The method is useful for diagnosis of inherited
 CC PAF-AH deficiency, which has been correlated with severe respiratory
 CC symptoms in asthmatic children. Recombinant PAF-AH can be used to treat
 CC inflammatory conditions.

XX Sequence 1520 BP; 452 A; 312 C; 332 G; 423 T; 1 other;

Query Match 99.7%; Score 1357.4; DB 18; Length 1520;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1358; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATGCAATGT 60
 DB 125 Tgagagactaagctgaaactgctgctgagctcccaagatggtgccacccaaattgcatgt 184
 QY 61 GCTTTTCGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 185 gctttctgctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 184
 QY 121 TCCGTGTCCTCATGAAATCATGAGTGGTCAACAAATACAAAGTACTGATGGCTGC 180
 DB 245 tccgtgtgctcatatgaaatcatgagatggtgctgctgctgctgctgctgctgctgctgct 304
 QY 181 TGCAGCTTTGCGCAAACTAAATCCCGGGGAATGGCCCTATTCCGTTGGTTGTAC 240
 DB 181 tgcagctttgcgcaaaactaaatcccggggaatggccctattccgttggttgtac 240

DB 305 tqcaagctttgcccacactaaatccccccggggaatgggcttattccgttgggtgtac 364
 QY 241 AGACTTAATGTTTGTACACTAATAAGGCGACACTCTTGGTGGTTATATATATCCATCCCA 300
 DB 365 agacttaattgttgatcacactaaatgaaggcacctcttcggtttattatccatccca 424
 QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
 DB 425 agataatgatcgcttgacacccctttggatccccaaataargaatattttggggtcttag 484
 QY 361 CAAATTTCTTGAACACACTGGCTTATGGCAACATTTTGGGTTACTCTTTGGTTCAT 420
 DB 485 caaattcttgaacacactgcttatgggcaacattttgaggtacctcttgggttcaat 544
 QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTTGGTGAATAATATCCACTTGTGT 480
 DB 545 gacaaactctgcaaaactggaattccctctgaggtcctggtgaaaaatataccactgtgtg 604
 QY 481 TTTTTCATGCTTGGGGCAATTCAGGACACTTTTATCTGCTATTGCGCATTGACCTGGC 540
 DB 605 tttttctcatggtccttgggcaatcaggacactttattctgctatttggcattggacctggc 664
 QY 541 ATCTCATGGGTTTATAGTTGCTGCTGAGAACACAGAGATAGATCTCATCTGCAACTTA 600
 DB 665 atctcatggtttatagttgctgctgtagaacaacagagatagatctgcatctgcaactta 724
 QY 601 CTATTTCAAGGACCACTCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
 DB 725 ctatttcaaggacccaatctgctgcagaaataggggcaagctcttggctctaccttagaac 784
 QY 661 CCTGAAACAGAGGAGGAGACACATATAGGAAATGAGCAGGTCACGCAAGAGCAAAAGA 720
 DB 785 cctgaaacaagaggagagacacatacacgaaatgagcaggcacggcaagagcaaaaga 844
 QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGTAAGAACCCAGTGAAGATGC 780
 DB 845 atgtcccaagctctcagctcgtattcttgacattcatctggaagcagtggaagatgc 904
 QY 781 ATTAGATTTAAAGTTTGTATGGAACACTGAAGACACTCTATTGTAGTGAAGAAATAGC 840
 DB 905 attagacttaagcttggataggaacttggaactggaagactctattgtagggaaaaatagc 964
 QY 841 AGTAATTTGGACATCTTTTGGTGAGCAACCGTTATTTCAGACTCTTACTGGAAGATCAGAG 900
 DB 965 agtaattggacattcttttggtagcaacggtattcagacctcttagtgaagatcagag 1024
 QY 901 ATTCAATGCTGATTTCCCTTGGATGATGATGATGATGATGATGATGATGATGATGATTC 960
 DB 1025 attcagatggtgattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1084
 QY 961 CAGAAATTCCTCAGCCCTCTTTTATCACTCTGAATATTTCCCAATATCTCTGCTAATAT 1020
 DB 1085 cagaattctcgaagccctctcttttatacactctgaaatttcccaatatactcgtcaatat 1144
 QY 1021 CATAAATTAAGAAATGCTACTCAGCTGATAAGAAAGAAAGATGATTACAAATCAGGGG 1080
 DB 1145 cataaaatgaaaaatgctactcactcactgataaagaaagaaagatgatacaaatcaggg 1204
 QY 1081 TTCAGTCCACCAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1205 ttcagttccaccagaaattttgctgacttcaacttttgcactggcgaataatattggacacat 1264
 QY 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAAATGCAGCTATTGCTTACCAATATCTCTGCTA 1200
 DB 1265 gctcaaattaagaggagacatagattcaaatgtagctattgactcttgcacaaagctc 1324
 QY 1201 ATTACATCTTTACAAAAGCAATTTAGACTTTCATTAAGATTTTGTATCAGTGGGACTGCTT 1260
 DB 1325 attagcattcttacaagaagcatttaggacttcaataaagattttgatcagtgaggactgctt 1384
 QY 1261 GATTCAAGGAGATGATGAGAATCTTATTCAGGGGCAACCAATTAACACACCAATCAACA 1320
 DB 1385 gattgaaggagatgatgagaaattcttattccaggggacaaacattaaacacacacaa 1444

QY 1321 CATCATCTTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1361
 Db 1445 catcatgtacagaactcttcagggaatagagaaacacaaatt 1485

RESULT 15

AAD04169
 ID AAD04169 standard; cDNA; 1320 BP.

XX AAD04169;

XX 02-JUL-2001 (first entry)

XX Mouse-Human plasma PAF-AH chimeric gene construct in plasmid pRC/PH.MHC2.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; chimeric; ss.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX Key location/Qualifiers

PH misc_feature 1..120

FT /*tag= a

FT /note= "Encodes N-terminal 40 amino acids of mouse
 platelet-activating factor acetylhydrolase (PAF-AH)."

FT misc_feature

FT 121..1320

FT /*tag= b

FT /note= "Encodes C-terminal 400 amino acids of human
 platelet-activating factor acetylhydrolase (PAF-AH)."

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

PR 22-JAN-1998; 98US-0010715.

PR 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

PI Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

PI Wilder CL;

XX WPI; 2001-280610/29.

DR P-PSDB; AAE00783.

XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF.

XX Example 8; Column -: 54pp; English.

XX The present cDNA sequence is mouse-human plasma platelet-activating
 CC factor acetylhydrolase (PAF-AH) chimeric gene construct in plasmid
 CC pRC/PH.MHC2.

CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicaemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX Sequence 1320 BP; 401 A; 269 C; 265 G; 385 T; 0 other;
 SQ

Query Match 91.7%; Score 1247.8; DB 22; Length 1320;
 Best Local Similarity 97.0%; Pred. No. 0;
 Matches 1283; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 38 ATGGTGCCACCCAAATTCGATGCTTTTCTGCTCGCGGCTCGCTGGCTGCTGCTTTAT 97
 Db 1 atgtaccactcaactcaggcgcttttctgctcctctgctgcctcccatgggtccat 60
 QY 98 CTTTTTGACGTGGCAATACATAAATCTCTGTTGCCCATATCAATCAATCAGCATGGTCAAC 157
 Db 61 ccttttcactggcaagacacatctctcttgg--actcaggcgctcagtaattttcac 117
 QY 158 AAATAACAGTACTGCTGCTGCAAGCTTTGGCCAACTTAAATCCCCCGGGGAAAT 217
 Db 118 aagatacaagactactgatgctgctgcaagcttttggccaaactaaatcccccggggaaat 177
 QY 218 GGGCCTTATTCGGTTCGTACAGACTTAATGTTTGTATCAGACTTAATAAGGGGACCTTC 277
 Db 178 gggccttattccgttgggtgtacagacttaattgtgatcacactaataagggcaccttc 237
 QY 278 TTGCGGTTTATATTCATCCATCCCAAGATAAATGATCGCTTGACACCTTTTGATGCCAAT 337
 Db 238 ttgcgtttatcatcatccatcccaagataatgatcgcttgcaccccttggatccccaaat 297
 QY 338 AAAGAATATTTTTGGGCTCTTAGCAAAATTTCTTGGAAACACACTGCTGCTTATGGCAACAT 397
 Db 298 aaagaatatatttggggtcttagcaaatcttctggagacacactgcttatgggcaacatt 357
 QY 398 TTGAGGTTACTCTTTGTTGTTCAATGACAACTCCTGCAAACTGGAAATCCCTCTGAGGCT 457
 Db 358 ttgaggttactcttgggttcaatgacaaactcctgcaaaactggaattccctctcctgagcct 417
 QY 458 GGTGAAAATATCCACTTGTGTTTCTCATGCTTTGGGGCATTCAGGACACTTTAT 517
 Db 418 ggtgaaaaatatccactctgtgttttctcatagctcttgaggacattcagacactttat 477
 QY 518 TCTGCTATTGGCAATGACCTGGCATCTCATGGGTTTATAGTTGTGCTGTAGAACACAGA 577
 Db 478 tctgctattggcattgacctggcactcactcctggtttatagttgctgctgtagaacacaga 537
 QY 578 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCACTCTGCTGCAGCAATAGGGGAC 637
 Db 538 gatagatctgcactctgcacttactatttcaaggaccacactctgctgcagaataaggggac 597
 QY 638 AAGTCTTGGCTCTACCTTAGAACCTGAAACAGAGAGGAGACACATATACGAATGAG 697
 Db 598 aagctctggctcctacccttagaacctcctgaaacagaggaggagacacatatcagaaatgag 657
 QY 698 CAGGTACGGCAAGAGACAAAGAATGTTCACCAAGCTCTCAGTCTGCTGCTTTGACATGAT 757
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 QY 938 CCATCGGCTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATTCACACTCTGAA 997
 Db 997

Db 898 ccaactgggtgatgaagtatatccagaattccctcagccccctcttttttatcaactctgaa 957
 QY 998 TATTTCCAATATCTGCTAATATCATATAAATAAATAAATGCTACTCCTCATATAAGAA 1057
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 Db 1018 agaaagatgattacaatcaggggttcagtcaccagaattttgtgacttcacttttgca 1077
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 QY 1358 AAT 1360
 Db 1318 aat 1320

Search completed: March 8, 2002, 23:08:27
 Job time: 3900 sec

LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
us-08-387-858A-9

Query Match 100.0%; Score 1361; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTGCACCCCAATTCATGT 60
Db 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTGCACCCCAATTCATGT 60
Qy 61 GCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 GCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 TCCTGTTCCCATATGAATCATCAGCATGGTCAACAAATACAAATGACTGCTGCTG 180
Db 121 TCCTGTTCCCATATGAATCATCAGCATGGTCAACAAATACAAATGACTGCTGCTG 180
Qy 181 TCGAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGAC 240
Db 181 TCGAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGAC 240
Qy 241 AGACTTAATGTTGATCAGCTAATGAAGGCACCTTCTGCGCTTATATATCCATCCA 300
Db 241 AGACTTAATGTTGATCAGCTAATGAAGGCACCTTCTGCGCTTATATATCCATCCA 300
Qy 301 AGATAATGATCCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTTAG 360
Db 301 AGATAATGATCCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTTAG 360
Qy 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Qy 421 GACAACTCTGCAAACTGGAATTCCTGCTGAGGCTGCTGGAATAATATCCACTTCTGT 480
Db 421 GACAACTCTGCAAACTGGAATTCCTGCTGAGGCTGCTGGAATAATATCCACTTCTGT 480
Qy 481 TTTTCTCATGCTTGGGGCAATTCAGGACACTTTATCTGCTATTTGGCATTTGACCTGGC 540
Db 481 TTTTCTCATGCTTGGGGCAATTCAGGACACTTTATCTGCTATTTGGCATTTGACCTGGC 540
Qy 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCAACTTA 600
Db 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCAACTTA 600
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAGCTTTGGCTCTACCTTAGAAC 660
Db 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAGCTTTGGCTCTACCTTAGAAC 660
Qy 661 CTTGAACAAAGAGGAGGACACATATACGAATGAGAGGTACGGCAAGAGCAAAAGA 720
Db 661 CTTGAACAAAGAGGAGGACACATATACGAATGAGAGGTACGGCAAGAGCAAAAGA 720
Qy 721 ATGTTTCCCAAGCTCTCAGTCTGATCTGATCTGACATTTGATATGGAAGCCAGTGAAGATGC 780
Db 721 ATGTTTCCCAAGCTCTCAGTCTGATCTGATCTGACATTTGATATGGAAGCCAGTGAAGATGC 780
Qy 781 ATTAGATTTAAAGTTTGAATGGAACAACTGAAGGACTCTATTGATGAGGAAAAATAGC 840
Db 781 ATTAGATTTAAAGTTTGAATGGAACAACTGAAGGACTCTATTGATGAGGAAAAATAGC 840
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Qy 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 900
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Qy 901 ATTCAGATGTGATTTGGCCCTGGATGCATGGATTTTCCACTGGTGATGAAGTATATTC 960
Db 901 ATTCAGATGTGATTTGGCCCTGGATGCATGGATTTTCCACTGGTGATGAAGTATATTC 960
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGAATAT 1020
Db 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGAATAT 1020
Qy 1021 CATATAAATGAAAAATGCTACTCAGCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Db 1021 CATATAAATGAAAAATGCTACTCAGCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Qy 1081 TTCAGTCCACCAAGATTTTCTGCTGACTTCACTTTTGGAACTGGCAAAATAATGGACACAT 1140
Db 1081 TTCAGTCCACCAAGATTTTCTGCTGACTTCACTTTTGGAACTGGCAAAATAATGGACACAT 1140
Qy 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCAGCTTATTGATCTTAGCAACAAGCTTC 1200
Db 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCAGCTTATTGATCTTAGCAACAAGCTTC 1200
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Db 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAT 1361
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RESULT 3

US-09-294-384B-9
; Sequence 9, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Glover, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,384B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:

NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1361 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 38..1360

US-09-294-384B-9

Query Match 100.0%; Score 1361; DB 4; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCACCCAAATTCATGT 60
DB 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGCACCCAAATTCATGT 60
QY 61 GCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 GCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 TCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 TCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 TCGAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTTATTCCTGCTGCTGCTGCT 240
DB 181 TCGAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTTATTCCTGCTGCTGCTGCT 240
QY 241 AGACTTAATGTTGATCAGCTAATGAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 AGACTTAATGTTGATCAGCTAATGAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 AGATAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 AGATAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CAAATTTCTTGAACACACACTGGCTTATGGGCAACATTTTTCAGGTTACTCTTTGGTTCAAT 420
DB 361 CAAATTTCTTGAACACACACTGGCTTATGGGCAACATTTTTCAGGTTACTCTTTGGTTCAAT 420
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGGAATATCCACTTGTGT 480
DB 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGGAATATCCACTTGTGT 480
QY 481 TTTTCTCATGCTTGGGGCACTTCAGGACACTTTTTCCTGCTTATGGCATTTGACCTGGC 540
DB 481 TTTTCTCATGCTTGGGGCACTTCAGGACACTTTTTCCTGCTTATGGCATTTGACCTGGC 540
QY 541 ATCTCATGGTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 ATCTCATGGTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTGCTCTACCTTAGAAC 660
DB 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTGCTCTACCTTAGAAC 660
QY 661 CCTGAAACAGAGGAGGACACATATAGGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
DB 661 CCTGAAACAGAGGAGGAGACACATATAGGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720

QY 721 ATGTTCCCAAGCTCTCAGCTTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
DB 721 ATGTTCCCAAGCTCTCAGCTTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
QY 781 ATTAGATTTAAAGTTTGAATGGAACAACACTGAAGGACTCTATTGATGAGGAAAAATAGC 840
DB 781 ATTAGATTTAAAGTTTGAATGGAACAACACTGAAGGACTCTATTGATGAGGAAAAATAGC 840
QY 841 AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAG 900
DB 841 AGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAG 900
QY 901 ATTGAGATGTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 ATTGAGATGTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTCAATATTTTCCAAATATCCTGCTAATAT 1020
DB 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTCAATATTTTCCAAATATCCTGCTAATAT 1020
QY 1021 CATAAAAATGAAAAATGCTACTCAGCTGATAAAGAAAGAAAGATGATTACAAATCAGGG 1080
DB 1021 CATAAAAATGAAAAATGCTACTCAGCTGATAAAGAAAGAAAGATGATTACAAATCAGGG 1080
QY 1081 TTCAGTCCACAGCAATTTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 TTCAGTCCACAGCAATTTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1200
DB 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1200
QY 1201 ATTGAGATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATGATGAGTGGACTGCTT 1260
DB 1201 ATTGAGATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATGATGAGTGGACTGCTT 1260
QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCCAGGAGCAACATTAACACAAACCAACA 1320
DB 1261 GATTGAAGGAGATGATGAGAAATCTTATTCCAGGAGCAACATTAACACAAACCAACA 1320
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
DB 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361

RESULT 4

US-08-470-187-7
; Sequence 7, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187

ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/318,905

FILING DATE: 6-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,803

FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5698403 and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32781

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1520 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 162..1484

US-08-483-140-7

Query Match 99.9%; Score 1359.4; DB 1; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCCCAAAATTCATGT 60
DB 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCCCAAAATTCATGT 184

QY 61 GCTTTTCTCCCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 185 GCTTTTCTCCCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244

QY 121 TCCTGTGGCCCATATGAATCATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 245 TCCTGTGGCCCATATGAATCATCATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 304

QY 181 TGCAAGCTTTGGCCAACTAAATATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 240
DB 305 TGCAAGCTTTGGCCAACTAAATATCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 364

QY 241 AGACATTAATGTTTGTATGACACTAATTAAGGCACTTCTTCGCTTATATATATATATATAT 300
DB 365 AGACATTAATGTTTGTATGACACTAATTAAGGCACTTCTTCGCTTATATATATATATATAT 424

QY 301 AGATAATGATCCCTTGACACCTTTTGGATCCCAATAAAGATAATTTTGGGCTCTTAG 360
DB 425 AGATAATGATCCCTTGACACCTTTTGGATCCCAATAAAGATAATTTTGGGCTCTTAG 484

QY 361 CAAATTTCTTGGACACACTGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAT 420
DB 485 CAAATTTCTTGGACACACTGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAT 544

QY 421 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCCCTGGTGAAAAATATCCACTGTTGT 480
DB 545 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCCCTGGTGAAAAATATCCACTGTTGT 604

QY 481 TTTTCTCATGCTCTTGGGCACTTCCAGACACTTTTATCTGCTATTGGCACTTGGACCTGGC 540
DB 605 TTTTCTCATGCTCTTGGGCACTTCCAGACACTTTTATCTGCTATTGGCACTTGGACCTGGC 664

QY 541 ATCTCATGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 600
DB 665 ATCTCATGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 724

QY 601 CTATTTCAAGGACCACTCTGCTGCAGAAATAGGGGCAAGCTTTGGCTCTACCTTGAAC 660
DB 725 CTATTTCAAGGACCACTCTGCTGCAGAAATAGGGGCAAGCTTTGGCTCTACCTTGAAC 784

QY 661 CCTGAAACAGAGGAGAGACACATATACGAATGACAGGATACGCCAAGAGCAAAAGA 720
DB 785 CCTGAAACAGAGGAGAGACACATATACGAATGACAGGATACGCCAAGAGCAAAAGA 844

QY 721 ATGTTCCCAAGCTCTCAGCTCTGATTTGACATTCATGATGAAAGCCAGTGAAGATGC 780
DB 845 ATGTTCCCAAGCTCTCAGCTCTGATTTGACATTCATGATGAAAGCCAGTGAAGATGC 904

QY 781 ATTAGATTTAAAGTTTGTATGGAACAACTGAAGACACTTATGATAGGAAAAAATAGC 840
DB 905 ATTAGATTTAAAGTTTGTATGGAACAACTGAAGACACTTATGATAGGAAAAAATAGC 964

QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTACAGACTCTTTAGTGAAGATCAGAG 900
DB 965 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTACAGACTCTTTAGTGAAGATCAGAG 1024

QY 901 ATTGAGATGTTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1025 ATTGAGATGTTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084

QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTCAATATTTCCCAATATCCCTGCTAATAT 1020
DB 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTCAATATTTCCCAATATCCCTGCTAATAT 1144

QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATTAAGAAAAAGAAAGATGATTACAAATCAGGGG 1080
DB 1145 CATAAAAATGAAAAATGCTACTCACCTGATTAAGAAAAAGAAAGATGATTACAAATCAGGGG 1204

QY 1081 TTCAGTCCCAAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1205 TTCAGTCCCAAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAAGATTTGATCTTAGCAACAAAGCTTC 1200
DB 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAAGATTTGATCTTAGCAACAAAGCTTC 1324

QY 1201 ATTAGATCTTTACAAAAGCATTTAGGACTTTCATTAAGATTTTGTAGTGGAGCTGCTT 1260
DB 1325 ATTAGATCTTTACAAAAGCATTTAGGACTTTCATTAAGATTTTGTAGTGGAGCTGCTT 1384

QY 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGAGCAACCAATTACACAAACCAATCAACA 1320
DB 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGAGCAACCAATTACACAAACCAATCAACA 1444

QY 1321 CATCATGTTTACAACTCTTTTTCAGGAATAGAGAAATACAATTT 1361
DB 1445 CATCATGTTTACAACTCTTTTTCAGGAATAGAGAAATACAATTT 1485

RESULT 8
US-08-485-938A-7
; Sequence 7, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.

APPLICANT: Gray, Patrick W.
 APPLICANT: Le Trong, Hai
 APPLICANT: Tjoelker, Larry W.
 APPLICANT: Wilder, Cheryl L.
 TITLE OF INVENTION: platelet-Activating Factor
 TITLE OF INVENTION: Acetylhydrolase
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, o'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-0402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,938A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,905
 FILING DATE: 06-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/133,803
 FILING DATE: 06-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5847088and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32792
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1520 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 162..1484
 95-08-485-938A-7

Query Match	99.9%	Score	1359.4	DB 2	Length	1520	
Best Local Similarity	99.9%	Pred.	No. 0				
Matches	1360	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
Qy	1	TCAGAGACTAAGCTGA	AACTGCTGCTCAGCTGCCAAGATGGTGGCACCCAAATTCG	CGTGT	60		
Db	125	TCAGAGACTAAGCTGA	AACTGCTGCTCAGCTGCCAAGATGGTGGCACCCAAATTCG	CGTGT	184		
Qy	61	GCTTTTCGCCCTCG	CGGCTCGCTTTCCTTTTGACTGGCAATACATAAA	120			
Db	185	GCTTTTCGCCCTCG	CGGCTCGCTTTCCTTTTGACTGGCAATACATAAA	244			
Qy	121	TCCTGTTGCCCATATGA	AATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	180			
Db	245	TCCTGTTGCCCATATGA	AATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	304			
Qy	181	TGCAAGCTTTTGCCCA	AACTAAATCCCCCGGGAAATGGGCCTTATCCGTTGGTTGTAC	240			
Db	305	TGCAAGCTTTTGCCCA	AACTAAATCCCCCGGGAAATGGGCCTTATCCGTTGGTTGTAC	364			
Qy	241	AGACTTAATGTTTGAT	CACACTAATAAGGGCACCTCTTGGGTTTATATTATTCATCCCA	300			
Db	365	AGACTTAATGTTTGAT	CACACTAATAAGGGCACCTCTTGGGTTTATATTATTCATCCCA	424			

Qy	301	AGATAATGATGCGCCTTGACACCCCTTTGGATCCCAATAAACAATATTTTGGGGCTCTTAG	360
Db	425	AGATAATGATGCGCCTTGACACCCCTTTGGATCCCAATAAACAATATTTTGGGGCTCTTAG	484
Qy	361	CAAAATTTCTTGGACACACACTGGCTTTATGGGCAACAATTTTGAGGTTACTCTTTGGTTGTC	420
Db	485	CAAAATTTCTTGGACACACACTGGCTTTATGGGCAACAATTTTGAGGTTACTCTTTGGTTGTC	544
Qy	421	GACAACTCCCTGCAAACTGGAAATCCCTCTGAGGCCTGGTGAAANAATATCCACTTGTGT	480
Db	545	GACAACTCCCTGCAAACTGGAAATCCCTCTGAGGCCTGGTGAAANAATATCCACTTGTGT	604
Qy	481	TTTTTCTCATGCTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCATTGACCTGGC	540
Db	605	TTTTTCTCATGCTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCATTGACCTGGC	664
Qy	541	ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCATGTCGAACCTTA	600
Db	665	ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCATGTCGAACCTTA	724
Qy	601	CTATTTCAAGGACCAATCTGCTGCGAANAATAGGGGACAAGTCTTGGCTCTACCTTTAGAAC	660
Db	725	CTATTTCAAGGACCAATCTGCTGCGAANAATAGGGGACAAGTCTTGGCTCTACCTTTAGAAC	784
Qy	661	CCTGAAACAAGGAGGAGACACATATACGAAATCAGCAGGTACGGCAAGACGAAAAGA	720
Db	785	CCTGAAACAAGGAGGAGACACATATACGAAATCAGCAGGTACGGCAAGACGAAAAGA	844
Qy	721	ATGTTCCCAAGCTCFCAGCTGTGATTTTGACATTCATCATGAGAACCCAGTGAAGATGC	780
Db	845	ATGTTCCCAAGCTCFCAGCTGTGATTTTGACATTCATCATGAGAACCCAGTGAAGATGC	904
Qy	781	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTTGATAGGGAATAATAGC	840
Db	905	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTTGATAGGGAATAATAGC	964
Qy	841	AGTAATTTGGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAG	900
Db	965	AGTAATTTGGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAG	1024
Qy	901	ATTCAGATGTGCTATTTGCCCTGGATGCCATGATTTCCACCTGGGTGATGAAGTATATTC	960
Db	1025	ATTCAGATGTGCTATTTGCCCTGGATGCCATGATTTCCACCTGGGTGATGAAGTATATTC	1084
Qy	961	CAGAAATCTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAAAT	1020
Db	1085	CAGAAATCTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAAAT	1144
Qy	1021	CATAAAAATGAAAAATGCTACTCACCTGATTAAGAAAGAAAGATGATTAACATCAGGG	1080
Db	1145	CATAAAAATGAAAAATGCTACTCACCTGATTAAGAAAGAAAGATGATTAACATCAGGG	1204
Qy	1081	TTTCAGTCCACCAAGAAATTTTGGCTGACTTTTTCACCTTTTGGCAACTGGCAAAATATTTGGACACAT	1140
Db	1205	TTTCAGTCCACCAAGAAATTTTGGCTGACTTTTTCACCTTTTGGCAACTGGCAAAATATTTGGACACAT	1264
Qy	1141	GCTCAAAATTAAGGGAGACATAGATTTCAAATGAGCTATTGATCTTTAGCAACAAGGCTTC	1200
Db	1265	GCTCAAAATTAAGGGAGACATAGATTTCAAATGAGCTATTGATCTTTAGCAACAAGGCTTC	1324
Qy	1201	ATTAGCATCTTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTTGATCAGTGGGACTGCTT	1260
Db	1325	ATTAGCATCTTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTTGATCAGTGGGACTGCTT	1384
Qy	1261	GATTCGAAGGAGATGATGAGAAATCTTATTCCAGGGGACCAACATTTAAGCAACCAATCAACA	1320
Db	1385	GATTCGAAGGAGATGATGAGAAATCTTATTCCAGGGGACCAACATTTAAGCAACCAATCAACA	1444
Qy	1321	CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT	1361
Db	1445	CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT	1485

RESULT 9
US-08-910-041-7
; Sequence 7, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tioelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-08-910-041-7

Query Match 99.9%; Score 1359.4; DB 2; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCCAAAATTCGATGT 60
DB 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCCAAAATTCGATGT 184
QY 61 GCTTTTCTGCTCGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120
DB 185 GCTTTTCTGCTCGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 244

121 TCCTGTTGCCCATATGAAATCATCAGCTGGCTCAACAAATACAAAGTACTGATGCTGC 180
DB 245 TCCTGTTGCCCATATGAAATCATCAGCTGGCTCAACAAATACAAAGTACTGATGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAAATCCCGGGGAAATGGCCCTTATTCCTGTTGGTGTAC 240
DB 305 TGCAAGCTTTGGCCAAACTAAAATCCCGGGGAAATGGCCCTTATTCCTGTTGGTGTAC 364
QY 241 AGACTTAATGTTTGATCACACTAATAAGGGACCTCTCTTGGCTTTATATATCAATCCCA 300
DB 365 AGACTTAATGTTTGATCACACTAATAAGGGACCTCTCTTGGCTTTATATATCAATCCCA 424
QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAG 360
DB 425 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAG 484
QY 361 CAAATTTCTTTGGAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTCAAT 420
DB 485 CAAATTTCTTTGGAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTCAAT 544
QY 421 GACAACCTCCGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 480
DB 545 GACAACCTCCGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 604
QY 481 TTTTCTCATGCTGCTGGGCACTTCAGGACACTTTTATTTCTGCTATTGGCATTCACCTGGC 540
DB 605 TTTTCTCATGCTGCTGGGCACTTCAGGACACTTTTATTTCTGCTATTGGCATTCACCTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCAATCTGCAACTTA 600
DB 665 ATCTCATGGGTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTCTGCGAGAAATAGGGGACAACTCTTGGCTCTACCTTAGAAC 660
DB 725 CTATTTCAAGGACCAATCTCTGCGAGAAATAGGGGACAACTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAGAGCAAAAGA 720
DB 785 CCTGAAACAAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTTGATGATGAAAGCAGTGAAGATGC 780
DB 845 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTTGATGATGAAAGCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGTATGGAACAACTCAAGGACCTCTTATGATAGGAAAAAATAGC 840
DB 905 ATTAGATTTAAAGTTTGTATGGAACAACTCAAGGACCTCTTATGATAGGAAAAAATAGC 964
QY 841 AGTAATTTGACATTTCTTTTGGTGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 900
DB 965 AGTAATTTGACATTTCTTTTGGTGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTCAGATGTTGTTATTTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
DB 1025 ATTCAGATGTTGTTATTTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTTGCCTAAAT 1020
DB 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTTGCCTAAAT 1144
QY 1021 CATAAAAATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAAATCAGGG 1080
DB 1145 CATAAAAATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAAATCAGGG 1204
QY 1081 TTCAGTCCACCAAGATTTTCTGCTCAGTCACTTTTGGCACTGGCAAAATATTTGGACACAT 1140
DB 1205 TTCAGTCCACCAAGATTTTCTGCTCAGTCACTTTTGGCACTGGCAAAATATTTGGACACAT 1264
QY 1141 GCTCAATTTAAAGGGAGACATAGATTCAAAATGAGCTTATGATCTTAGCAACAAAGCTTC 1200
DB 1265 GCTCAATTTAAAGGGAGACATAGATTCAAAATGAGCTTATGATCTTAGCAACAAAGCTTC 1324
QY 1201 ATTACATTTCTTACAAAAAGCATTTAGGACTTTCATAAAGATTTTGTATCAGTGGGACTGCTT 1260

Db 1325 ATTAGCATCTTACAAAGCATTTAGGACTTCATAAAGATTTGATCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 10

US-09-328-474-7
; Sequence 7, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/328,474
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rio-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484

US-09-328-474-7

Query Match 99.9% Score 1359.4; DB 3; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAAGCTGCTCAGCTCCCAAGATGGTCCCAACCCCAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAAGCTGCTCAGCTCCCAAGATGGTCCCAACCCCAATTCATGT 184
Qy 61 GCTTTTCTGCCTCTGCGGCTGCTGGCTGTGGTTTATCTCTTTTGACHTGGCAATACATAA 120
Db 185 GCTTTTCTGCCTCTGCGGCTGCTGGCTGTGGTTTATCTCTTTTGACHTGGCAATACATAA 244
Qy 121 TCCTGTTGCCCATATGAAATCATCAGCATGGTCAACAAATACAAATACAAATGCTGC 180
Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGTCAACAAATACAAATACAAATGCTGC 304
Qy 181 TGAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGCCCTTATTCCGTTGGTTGTAC 240
Db 305 TGAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGCCCTTATTCCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTGATCACACTAATAAGGGCACCTTCTTGGCTTATATTTATCCATCCCA 300
Db 365 AGACTTAATGTTGATCACACTAATAAGGGCACCTTCTTGGCTTATATTTATCCATCCCA 424
Qy 301 AGATAATGATCGCTTGCACACCTTTGATCCCAAAATAAAGAAATATTTTGGGGCTTTAG 360
Db 425 AGATAATGATCGCTTGCACACCTTTGATCCCAAAATAAAGAAATATTTTGGGGCTTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCCTGCAAACTGGAAATCCCTCTCAGGCTGGTCAAAATATCCACTTTGTTGT 480
Db 545 GACAACTCCTGCAAACTGGAAATCCCTCTCAGGCTGGTCAAAATATCCACTTTGTTGT 604
Qy 481 TTTTCTCATGGTCTTGGGCACTTTCAGGACACTTTTATCTGCTATGTCATTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGCACTTTCAGGACACTTTTATCTGCTATGTCATTGACCTGGC 664
Qy 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACAAAGCTTTGGCTCTACCTTAGAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACAAAGCTTTGGCTCTACCTTAGAC 784
Qy 661 CCTGAACAAGGAGGAGACACATATACGAAATGAGGAGTACGCAAGGACCAAGCA 720
Db 785 CCTGAACAAGGAGGAGGAGACACATATACGAAATGAGGAGTACGCAAGGACCAAGCA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGATCATGATGAAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGATCATGATGAAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTTATGATGGAACAACTGAAGGACTCTATTGATAGGAAATAATAGC 840
Db 905 ATTAGATTTAAAGTTTATGATGGAACAACTGAAGGACTCTATTGATAGGAAATAATAGC 964
Qy 841 AGTAATTCGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGTACAG 900
Db 965 AGTAATTCGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGTACAG 1024
Qy 901 ATTCAGATGTGATTTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGATTTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTCTAATAT 1020
Db 1085 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTCTAATAT 1144
Qy 1021 CATAAAAATGAAAAAATGCTACTCAGCTGATAAAGAAAGAGATGATTACAATCAGGG 1080

Db 1145 CATAAAATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAAATCAGGG 1204
QY 1081 TTCAGTCACACAGAAATTTGCTGACTTCACCTTTTGCACCTGCGAAATATTTGGACACAT 1140
Db 1205 TTCAGTCACACAGAAATTTGCTGACTTCACCTTTTGCACCTGCGAAATATTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAATCGAGCTATTGATCTTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAATCGAGCTATTGATCTTTAGCAACAAAGCTTC 1324
QY 1201 ATTAGCATCTTACAAAGAGCTTTAGGACTTCATAAAGATTTTGTAGCTGGACCTGCTT 1260
Db 1325 ATTAGCATCTTACAAAGAGCTTTAGGACTTCATAAAGATTTTGTAGCTGGACCTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGGAGACCAACATTAACACACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGGAGACCAACATTAACACACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1485

RESULT 11

US-09-100-546-7
; Sequence 7, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-09-100-546-7

Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCGATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCGATGT 184
QY 61 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAATACAA 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAATACAA 304
QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCCTGTTGGTCTTAC 240
Db 305 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCCTGTTGGTCTTAC 364
QY 241 AGACTTAATGTTTGATCACACTTAATAAGGGCACCTCTTTCGGCTTATATATATATATATAT 300
Db 365 AGACTTAATGTTTGATCACACTTAATAAGGGCACCTCTTTCGGCTTATATATATATATATAT 424
QY 301 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTTGGTGAATAATATCCACTCTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTTGGTGAATAATATCCACTCTGTGT 604
QY 481 TTTTCTCATGCTGCTGGGCAATTCAGGACACTTTTATCTGCTATTTGGCATTTGACCTGGC 540
Db 605 TTTTCTCATGCTGCTGGGCAATTCAGGACACTTTTATCTGCTATTTGGCATTTGACCTGGC 664
QY 541 ATCTCATGGCTTTTATAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 665 ATCTCATGGCTTTTATAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 724
QY 601 CTATTTCAAGGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 725 CTATTTCAAGGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784
QY 661 CCTGAAACAGAGAGGAGACACATATACGAATAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAGAGAGGAGAGACACATATACGAATAGCAGGTACGGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 780
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QY 781 ATTAGATTTAAAGTTTGTATATGGAACAACTGAAGGACTCTATTGATAGGAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGTATATGGAACAACTGAAGGACTCTATTGATAGGAAAAATAGC 964
QY 841 AGTAATTTGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAG 900
Db 965 AGTAATTTGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAG 1024

QY 781 ATTAGATTTAAAGTTTGATATGAACAACCTGAAGGACTCTATTGATAGGAGAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGAACAACCTGAAGGACTCTATTGATAGGAGAAAAATAGC 964
QY 841 AGTAATTGGACATCTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATCTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 1024
QY 901 ATTACAGATGTGGTATTGCGCTGGATGATGATGTTTCCACCTGGGTGATGAAGTATATTC 960
Db 1025 ATTACAGATGTGGTATTGCGCTGGATGATGATGTTTCCACCTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAATGCTACTCACCCTGATTAAGAAAGAAAGATGATTACAAATCAGGG 1080
Db 1145 CATAAAAATGAAAAATGCTACTCACCCTGATTAAGAAAGAAAGATGATTACAAATCAGGG 1204
QY 1081 TTCAGTCCACAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATATTTGGACACAT 1140
Db 1205 TTCAGTCCACAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATATTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGAGACATAGATTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTC 1200
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QY 1201 ATTAGCATCTTCAAAAGCAATTTAGGACTTCATTAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATCTTCAAAAGCAATTTAGGACTTCATTAAGATTTTGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGAGATGATGAGAAATCTTTATCCAGGACCAACATTAACAAACCAATCAACA 1320
Db 1385 GATTGAAGAGATGATGAGAAATCTTTATCCAGGACCAACATTAACAAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 13

US-09-577-758-7
; Sequence 7, Application US/0957758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hal
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
; US-09-577-758-7

Query Match 99.9%; Score 1359.4; DB 4; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAAGTCTGCTCAGCTCCCAAGATGGTCCCAACCAAAATTCGATGT 60
Db 125 TGAGAGACTAAGCTGAAAGTCTGCTCAGCTCCCAAGATGGTCCCAACCAAAATTCGATGT 184
QY 61 GCCTTTCTGCTCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCCTTTCTGCTCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGC 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAAATCCCGGGGAAATGGGCTTATTCGGTGGTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAAATCCCGGGGAAATGGGCTTATTCGGTGGTGTAC 364
QY 241 AGACTTAATGTTGATCACACTAATAAGGCAACCTTCCTGCTTTATATATATCCATCCCA 300
Db 365 AGACTTAATGTTGATCACACTAATAAGGCAACCTTCCTGCTTTATATATATCCATCCCA 424
QY 301 AGATAATGATCGCTTCACACCCCTTTGGATCCCAAAATAAAGAAATATTTTGGGCTCTAG 360
Db 425 AGATAATGATCGCTTCACACCCCTTTGGATCCCAAAATAAAGAAATATTTTGGGCTCTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAT 544
QY 421 GACAACCTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAGAAATATCCACTTGTGT 480
Db 545 GACAACCTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAGAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGTTCTTGGGGCATTCAGGACACTTTATTCCTATTTGGCATTTGACCTGGC 540
Db 605 TTTTCTCATGTTCTTGGGGCATTCAGGACACTTTATTCCTATTTGGCATTTGACCTGGC 664
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATCTGCAACTTA 600
Db 665 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 784

QY 638 AAGTCTGGCTCTACCTTAGAACCTGAAACAGAGGAGGAGACACATATACGAAATGAG 697
Db 601 AAGTCTGGCTCTACCTTAGAACCTGAAACAGAGGAGGAGACACATATACGAAATGAG 660
QY 698 CAGGTACGCGCAAGAGCAAGAAATGTTCCCAAGCTCTCAGTCTGATCTTGCATTTGAT 757
Db 661 CAGGTACGCGCAAGAGCAAGAAATGTTCCCAAGCTCTCAGTCTGATCTTGCATTTGAT 720
QY 758 CATGGAAGCCAGTGAAGATGCAATAGATTTAAAGTCTTGTATGCAACAACTGAAGGAC 817
Db 721 CATGGAAGCCAGTGAAGATGCAATAGATTTAAAGTCTTGTATGCAACAACTGAAGGAC 780
QY 818 TCTATTGATAGGGAAGAAATAGCAGTAATGAGCAATCTTTTGGTGAGCAACGGTTATT 877
Db 781 TCTATTGATAGGGAAGAAATAGCAGTAATGAGCAATCTTTTGGTGAGCAACGGTTATT 840
QY 878 CAGACTCTTAGTGAAGATCAGAGATTCAGATCTGATGCTGATTTGCCCTGGATCGATGGATTT 937
Db 841 CAGACTCTTAGTGAAGATCAGAGATTCAGATCTGATGCTGATTTGCCCTGGATCGATGGATTT 900
QY 938 CCACTGGGTGATGAAGTATATTCAGAAATCTCTCAGCCCTCTTTTATCAACTCTGAA 997
Db 901 CCACTGGGTGATGAAGTATATTCAGAAATCTCTCAGCCCTCTTTTATCAACTCTGAA 960
QY 998 TATTTCCAATATCTGCTAATATCATAAATGAAAAATGCTACTCACTCATGATAAGAA 1057
Db 961 TATTTCCAATATCTGCTAATATCATAAATGAAAAATGCTACTCACTCATGATAAGAA 1020
QY 1058 AGAAGATGATTAACAATCAGGGTTCAGTCCACCAAGATTTTGTGACTTCACTTTTGA 1117
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QY 1118 ACTGGCAAAATATGAGACATGCTCAAAATTAAGGAGAGACATAGATTTCAATCCAGCT 1177
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QY 1178 ATTGATCTTAGCAACAAGCTTCAATAGCATCTTACAAAGCATTTAGGACTTCATAAA 1237
Db 1141 ATTGATCTTAGCAACAAGCTTCAATAGCATCTTACAAAGCATTTAGGACTTCATAAA 1200
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Db 1201 GATTTTGATCAGTGGGACTGCTTGAATGAAGGAGATGATGAGATCTTATTCAGGGACC 1260
QY 1298 ACATTAACACACCAATCAACATCATGTTACAGAACTCTTACAGGAATAGAGAAATAC 1357
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QY 1358 AATT 1361
Db 1321 AATT 1324

RESULT 15

US-08-485-938A-30
; Sequence 30, Application US/08485938A
; Patent No. 5847088

GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-485-938A-30

Query Match 85.4%; Score 1162.4; DB 2; Length 1335;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 38 ATGGTGGCCACCCCAATTTGCATGTGCTTTTCTGCGCTCTGCGGCTGCGTGTGCTGTGTTAT 97
Db 1 ATGGTACCCCAAGAGCTGCAGCTGCTGTTTGTCTGTGTGATGTCTCCCGCTGCTGTAC 60
QY 98 CTTTGTGACGTGGCAATACATAAATCCCTGTGCCCATAATGAAATCATCAGCATGGGTCAAC 157
Db 61 CCCTTCGATGGCAGTATATCAACCCGCTGCTCATGAGAGCAGCCCTGGGTGAAT 120
QY 158 AAAATACAAGTACTGATGGCTGTGCAAGCTTTGGCCCAAACTAAAATCCCCGGGGAAT 217
Db 121 AAGATCCAGGTGCTCATGGCGCCACCAAGCTTGGGTGAGCAAGATTCCTAGAGGCAAC 180
QY 218 GGGCCCTATTCCGTTGGTGTACAGACTTAATGTTGATCAGACTTAATAAGGCGACCTTC 277
Db 181 GGGCCCTACAGCGTGGGCTGCACGATCTGATGTTGCGACCATACCAACAAAGAACTTT 240
QY 278 TTGCGTTTATATTATCCATCCCAAGATAATGATGCGCTTGACACCTTTGGATCCCAAT 337
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QY 338 AAAGAATATTTTGGGCTCTTAGCAAAATTTCTTGAACACACTGGCTTATGGGCAACATT 397
Db 301 AAAGAATATTTTGGGCTCTTAGCAAAATTTCTTGAACACACTGGCTTATGGGCAACATT 360
QY 398 TTGAGGTACTCTTTGTTTCAATCACAACCTCTCAAACTGGAATTCCTCTGAGGCT 457
Db 361 TTGAGGTACTCTTTGTTTCAATCACAACCTCTCAAACTGGAATTCCTCTGAGGCT 420
QY 458 GTGAAAAATATCCACTTGTGTTTCTATGCTGTGGGCACTTCAGGACACTTAT 517
Db 421 GTGAAAAATATCCACTTGTGTTTCTATGCTGTGGGCACTTCAGGACACTTAT 480
QY 518 TCTGCTATTGGCATTCACCTGGCATCTCATGGTGTAGTTGCTGCTGTAGAACACAGA 577
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Db 481 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTAGAACACAGA 540
QY 578 GATAGATCTGCATCTGCAACTTACTATTTCAGAGACCAATCTGCTGCACAAATAGGGGAC 637
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Db 1321 AATT 1324

Search completed: March 8, 2002, 23:05:20
Job time: 3863 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:47:12 ; Search time 1552.89 seconds
(without alignments)
9417.927 Million cell updates/sec

Title: US-09-922-067-9

Perfect score: 1361

Sequence: 1 TCAGAGACTAAGCTGAACT.....AGGAATAGAGAAATCAATT 1361

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST.*
- 1: em_estfun.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estom.*
 - 5: em_estpl.*
 - 6: em_estba.*
 - 7: em_estro.*
 - 8: em_estov.*
 - 9: em_hic.*
 - 10: gb_estl.*
 - 11: gb_est2.*
 - 12: gb_hic.*
 - 13: gb_gss.*
 - 14: em_gss_fun.*
 - 15: em_gss_hum.*
 - 16: em_gss_inv.*
 - 17: em_gss_pln.*
 - 18: em_gss_pro.*
 - 19: em_gss_rod.*
 - 20: em_gss_vrt.*
 - 21: em_gss_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	912.6	67.1	932	10	AL575852
C 2	854.6	62.8	978	10	AL554852
C 3	822.2	60.4	875	10	AL573565
C 4	785.2	57.7	1693	12	AK005210
C 5	758.6	55.7	991	10	AL552617
C 6	716.5	52.6	893	10	AL549288
C 7	643.6	47.3	1376	12	AK005158
C 8	590.2	43.4	900	11	BG530083
C 9	571.2	42.0	650	10	AI343491
C 10	529.6	38.9	874	11	BI182205
C 11	513.6	37.7	598	11	BF509203
C 12	497.4	36.5	519	10	AW071677

C 13	483.8	35.5	560	11	BF508812
C 14	436.4	32.1	817	11	BI159467
C 15	420	30.9	851	11	BG918925
C 16	400.8	29.4	642	11	BI146868
C 17	390.6	28.7	628	10	AW911082
C 18	390.2	28.7	420	10	AA302965
C 19	379.2	27.9	928	11	BG519457
C 20	372.4	27.4	827	11	BG921765
C 21	370	27.2	394	10	AI177011
C 22	364.8	26.8	816	10	AU080891
C 23	359.8	26.4	541	10	AW321503
C 24	356.4	26.2	663	10	AA183265
C 25	353.8	26.0	453	10	AW461498
C 26	342.4	25.2	898	11	BI105479
C 27	340.2	25.0	898	11	BG923882
C 28	333.2	24.5	669	10	BE303582
C 29	331.4	24.3	828	11	BG917419
C 30	325.4	23.9	732	11	BE850256
C 31	324.6	23.9	803	10	BE569215
C 32	322.4	23.7	513	10	AW950435
C 33	315.2	23.2	807	10	AI136371
C 34	305.8	22.5	477	11	BI133781
C 35	304.8	22.4	656	11	BF144748
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C 37	304	22.3	720	10	AU067449
C 38	302.8	22.2	379	10	AA297235
C 39	302.4	22.2	537	10	BE281780
C 40	301	22.1	454	10	BE227253
C 41	297.6	21.9	441	11	BF225052
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C 43	294.8	21.7	466	10	BE291982
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C 45	292.2	21.5	765	10	BE535154

ALIGNMENTS

RESULT 1
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LOCUS AL575852 932 bp mRNA 16-FEB-2001
DEFINITION AL575852 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1067YM18 3 prime, mRNA sequence.
ACCESSION AL575852
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 255 a 190 c 181 g 299 t 7 others

Query Match 67.1%; Score 912.6; DB 10; Length 932;
Best Local Similarity 98.2%; Pred. No. 6.2e-218;
Matches 915; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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RESULT 2

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LOCUS AL554852 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI087YO19 5
DEFINITION prime, mRNA sequence.
ACCESSION AL554852
VERSION AL554852.1 GI:12896029
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 978)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source

1..978
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/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 253 a 216 c 237 g 270 t 2 others
ORIGIN

Query Match 62.8%; Score 854.6; DB 10; Length 978;
Best Local Similarity 99.3%; Pred No. 2.1e-203;
Matches 857; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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ACCESSION AL573565
VERSION AL573565.1 GI:12932922
KEYWORDS EST.
SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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BASE COUNT 227 a 187 c 166 g 263 t 32 others

ORIGIN

Query Match 60.4%; Score 822.2; DB 10; Length 875;
Best Local Similarity 94.3%; Pred. No. 2.6e-195;
Matches 825; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
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RESULT 4

LOCUS AK005210
DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500011H20, full insert sequence.
AK005210 1695 bp mRNA HTC 05-JUL-2001
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500011H20, full insert sequence.

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com

BASE COUNT 244 a 248 c 246 g 251 t 2 others
ORIGIN

Query Match 55.7% Score 758.6; DB 10; Length 991;
Best Local Similarity 99.0%; Pred. No. 2.2e-179;
Matches 783; Conservative 1; Mismatches 5; Indels 2; Gaps 2;

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DB 323 TCCTGTTGCCCATATGAATCATCAGCATGGTCAACAAATACAAAGTACTGATGCTGC 382
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGGTGGTGTAC 240
DB 383 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGGTGGTGTAC 442
QY 241 AGACTTAATGTTTGCATCACACTAATAAGGGACCTTCTTGGCTTTATATATCCATCCCA 300
DB 443 AGACTTAATGTTTGCATCACACTAATAAGGGACCTTCTTGGCTTTATATATCCATCCCA 502
QY 301 AGATAATGATCGCCTTGACACCTTTGGATCCCAATAAAGATATTTTGGGGTCTTAG 360
DB 503 AGATAATGATCGCCTTGACACCTTTGGATCCCAATAAAGATATTTTGGGGTCTTAG 562
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTCAAT 420
DB 563 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTCAAT 622
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGTGTAATAATATCCACTTGTGT 480
DB 623 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGTGTAATAATATCCACTTGTGT 682
QY 481 TTTTCTCATGCTCTTGGGGCATTCAGGACCTTTATCTGCTTATTTGGCATTCACCTGGC 540
DB 683 TTTTCTCATGCTCTTGGGGCATTCAGGACCTTTATCTGCTTATTTGGCATTCACCTGGC 742
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DB 743 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCACTTA 802
QY 601 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
DB 803 CTATTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 862
QY 561 CCTGAACAAGAGGAGAGACACATATACGAATGAGAGGTACGCGCAAGAGCAAGA 720
DB 863 CTGAACAAGAGGAGAGACACATATACGAATGAGAGGTACGCGCAAGAGCAAGA 922
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTGCATTTGATCATGGAAGCCAGTGAAGATGC 780
DB 923 ATGTTCCCAAGCTCTCAGTCTGATTTTGCATTTGATCATGGAAG - ATGC 980
QY 781 ATTAGATTAA 791
DB 981 ATTAGATTAA 991

RESULT 6
AL549288

784 AGATTTAAAGTTTATATGATGAACAACTGAAGGACTCTTATTCATAGGGGAAATAATAGCACT 843
DB 909 AG-TTTTCACTTTGACATGAACAGCTGAGGATGCTTATTCATGAGACTAAATAGCTTT 967
QY 844 AATTGGACATCTTTTGGTGGAGCAACGGTTATTCAGACCTTCTAGTGAAGATTCAGAGATT 903
DB 968 GATGGACATCTTTTGGAGGAGCAACAGTTCTTCAAGCCCTTASTGAGGACCAAGAGATT 1027
QY 904 CAGATGCTGATTTGCCCTGGATCATGGATGTTTCCACTGGGTGATGAAGTATATTCAG 963
DB 1028 CAGATGCTGATTTGCCCTGGATCATGGATGTTTCCACTGGGTGATGAAGTATATTCAG 1087
QY 964 AATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTGCTTAATATCAT 1023
DB 1088 AACCTTCCAGCTCTCTCTTTTCAACTCTGCCAATTCAGACTTCCAAAGGACATCGC 1147
QY 1024 AAAAATGAAAATGCTACTACCTGATTAAGAAAGAAAGATGATTAACAACTCAGGGTTC 1083
DB 1148 AAAAATGAAAATGCTACTACCTGATTAAGAAAGAAAGATGATTAACAACTCAGGGTTC 1207
QY 1084 ACTCCACCAAGATTTTGGCTGACCTTCACTTTTGAACCTGGCAAAATATTTGGACACATGCT 1143
DB 1208 AGTGACCAAGACTTTTGGACCTTCACTTTTGAACCTGGCAAAATATTTGGAAACAACT 1267
QY 1144 CAAATTAAGGGAGACATGATTAATCAATGACAGCTTATTCATCTTAGCAACAAAGCTTTCATT 1203
DB 1268 GACACTGAAGGAGAAATCGATTTCCAGATGAGCATCGACTCCCAACAAAGCTTCGAT 1327
QY 1204 AGATTTTACAAAAGCAATTTAGACCTTCAATAAGATTTTGTAGTGGGACTGCTGAT 1263
DB 1328 GGCTTTTCAAAAAGCAATTTAGGCTTCAAAAAGCAATTTGATCAGTGGGACCTCTGCT 1387
QY 1264 TGAAGGATGATGAGAACTTTATTCAGGGCAACAACTTAACACAACTCAACACAT 1323
DB 1388 GGAAGGATGATGAGAACTTTATTCAGGGCAACAACTTAACACAACTCAACACAT 1447
QY 1324 CATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361
DB 1448 GGCTCAGCAACACTCTCCAGGATCAGACAGCCAGAAAT 1485

RESULT 5
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LOCUS AL552617 991 bp mRNA EST 16-FEB-2001
DEFINITION AL552617 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1067YM18 5
prime, mRNA sequence.
ACCESSION AL552617
VERSION AL552617.1 GI:12891690
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .991
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1067YM18"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6

FEATURES
Source

LOCUS AL549288 893 bp mRNA EST 16-FEB-2001
 DEFINITION AL549288 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1049YE02 5
 prime, mRNA sequence.
 ACCESSION AL549288
 VERSION AL549288.1 GI:12885119
 KEYWORDS EST.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 893)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 Location/Qualifiers
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 215 a 222 g 230 t 1 others
 ORIGIN
 Query Match 52.6%; Score 716; DB 10; Length 893;
 Best Local Similarity 99.7%; Pred. No. 1e-168;
 Matches 716; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGAGAGACTAAGCTGAACCTGCTGCTAGCTCCCAAGATGGTGCCACCAAAATTCATGT 60
 Db 176 TGAGAGACTAAGCTGAACCTGCTGCTAGCTCCCAAGATGGTGCCACCAAAATTCATGT 235
 QY 61 GCTTTTCTGCTCTGCGGCTGCCCTGCTGCTGCTTTATCTTTGACTGGCAATACATAAA 120
 Db 236 GCTTTTCTGCTCTGCGGCTGCCCTGCTGCTGCTTTATCTTTGACTGGCAATACATAAA 295
 QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
 Db 296 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 355
 QY 181 TGCAAGCTTGGCCCAACTAAATCCCCCGGGGAATGGGCTTATCCGTTGGTTGTAC 240
 Db 356 TGCAAGCTTGGCCCAACTAAATCCCCCGGGGAATGGGCTTATCCGTTGGTTGTAC 415
 QY 241 AGACTTAAATGTTTGATCACACTAATAAGGACCTCTCTGCGTTTATATATTCATCCATCCCA 300
 Db 416 AGACTTAAATGTTTGATCACACTAATAAGGACCTCTCTGCGTTTATATATTCATCCATCCCA 475
 QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAAAATTAAGAATATTTTGGGCTCTTAG 360
 Db 476 AGATAATGATCGCTTGACACCTTTGGATCCCAAAATTAAGAATATTTTGGGCTCTTAG 535
 QY 361 CAAATTTCTTGGACACACTGGCTTATGGCAACATTTTGGAGTACTCTTTGGTTCAAT 420
 Db 536 CAAATTTCTTGGACACACTGGCTTATGGCAACATTTTGGAGTACTCTTTGGTTCAAT 595
 QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGCGCTGGTGAATAATATCCACTTGTGT 480

Db 596 GACAACTCTGCAAACTGGAATTCCTCTGAGCGCTGGTGAATAATATCCACTTGTGT 655
 QY 481 TTTTCTCATGCTGCTTGGGCATTCAGGACACTTATTCGCTATTCGATTCAGCTGGC 540
 Db 656 TTTTCTCATGCTGCTTGGGCATTCAGGACACTTATTCGCTATTCGATTCAGCTGGC 715
 QY 541 ATCTCATGGTGTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATTCGCAACTTA 600
 Db 716 ATCTCATGGTGTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATTCGCAACTTA 775
 QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGCTTTGGCTCTACCTTAGAAC 660
 Db 776 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGCTTTGGCTCTACCTTAGAAC 835
 QY 661 CCTGAACAAGAGGAGGAGACACATATACGAATAGCAGGTAGCGGCAAGAGCAAAA 718
 Db 836 CTTGAACAAGAGGAGGAGACACATATACGAATAGCAGGTAGCGGCAAGAGCAAAA 893
 RESULT 7
 LOCUS AK005158 1376 bp mRNA HTC 05-JUL-2001
 DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
 library, clone:1500005E13, full insert sequence.
 ACCESSION AK005158
 VERSION AK005158.1 GI:12836890
 KEYWORDS CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA,
 clone:lib:RIKEN full-length enriched mouse cDNA library
 clone:1500005E13.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1376)
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Methods in enzymology. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2 (bases 1 to 1376)
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, N., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome research. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3 (bases 1 to 1376)
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome research. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4 (bases 1 to 1376)
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5 (bases 1 to 1376)
 AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
 Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,
 Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P.,
 Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J.,
 Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
 Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
 Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,

Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 5'-GAGAGAGAGAGCGGCGCAATTAATCTCGAGTTAAATTAATCCCCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

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 /clone="1500005E13"
 /sex="male"
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 AIGGLASNGIVATVERDRSASATYFEDQVAAKVNRSLYLKVKQESSEVRK
 EQVOARTECSRALSAILDIEHGDPRKNVLGSFDMKQLDAIDETKIALMHGFSFGA
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 QPDKERKMITIK"

BASE COUNT 380 a 298 c 311 g 387 t

Query Match 47.3%; Score 643.6; DB 12; Length 1376;

Best Local Similarity 75.6%; Pred. No. 1.4e-150;
 Matches 812; Conservative 0; Mismatches 259; Indels 3; Gaps 1;

QY 5 ACAGTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTCATGCTCTT 64
 Db 75 ACATCAAACTGAAGCCACTGCTGCTCCTTAAGATGGTACCACTCAAACTGCAGGCGCTT 134
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 Db 195 TTGTG--ACTTCAGGCGGTCAGTAATGTTTCACAAGCTCCAACTCGGTGATGCTGCTGCC 251
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 Db 252 GGCTCTGGCCATAGTAAATCCCAAGGAATGGATCGTACCCCGCTCGGTTGTACAGAT 311

QY 245 TTAATGTTTATGATCACACTAATAAGGGCACCTTCTTGGCTTTATATTTATCCATCCCAAGAT 304
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 QY 305 AATGATGCGCTTGACACCCCTTTGGATCCCAATAAAGAATAATTTTGGGTCTTTAGCAAA 364
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 Db 552 TCTCATGCTCTCGAGGCTTTCAGGACCAATTTATTTCTGCTATTTGGCAATTTGGCATCT 611
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 Db 972 AGATGCTGAGTCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1031
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RESULT 8

LOCUS BG530083 900 bp mRNA EST 03-APR-2001
 DEFINITION 602558743F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:469691 5', mRNA sequence.
 ACCESSION BG530083
 VERSION BG530083.1 GI:13521620
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 900)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1524 row: e column: 12
High quality sequence stop: 628.

FEATURES

source

1. 900
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/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGCCGCGCGGCGACATG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 305 a 144 c 215 g 236 t
ORIGIN

Query Match 43.4%; Score 590.2; DB 11; Length 900;
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Matches 630; Conservative 0; Mismatches 8; Indels 5; Gaps 3;

QY 670 AGAGGAGGAGACACATATAGCAATGAGCAGGTACGCCAAGAGCAAAAGAAATGTTCCCA 729
DB 1 AGAGGAGGAGACACATATAGCAATGAGCAGGTACGCCAAGAGCAAAAGAAATGTTCCCA 60

QY 730 AGCTCTCAGTCTGATTTGACATTCATGATGGAAGCCAGTGAAGATGATGATTT 789
DB 61 AGCTCTCAGTCTGATTTGACATTCATGATGGAAGCCAGTGAAGATGATGATTT 120

QY 790 AAAGTTTGATGGAACAACACTGAAGACTCTATTGATAGGAAAAAATAGCAATGCG 849
DB 121 AAAGTTTGATGGAACAACACTGAAGACTCTATTGATAGGAAAAAATAGCAATGCG 180

QY 850 ACATCTCTTTGGTGGAGCAACGGTTATTCAGACTCTTATGCAAGATCAGAGATTCAGATG 909
DB 181 ACATCTCTTTGGTGGAGCAACGGTTATTCAGACTCTTATGCAAGATCAGAGATTCAGATG 240

QY 910 TGGTATGCCCCTGGATGCGATGTTTCCACTGGGTGATGAGTATATTCAGAAATCC 969
DB 241 TGGTATGCCCCTGGATGCGATGTTTCCACTGGGTGATGAGTATATTCAGAAATCC 300

QY 970 TCAGCCCTCTTTTATCACTCTCAATATTTCCAAATATTCCTGCTAATATCAATAAAT 1029
DB 301 TCAGCCCTCTTTTATCACTCTCAATATTTCCAAATATTCCTGCTAATATCAATAAAT 360

QY 1030 GAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAAATCAGGGTTCCAGTCCA 1089
DB 361 GAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAAATCAGGGTTCCAGTCCA 420

QY 1090 CCAGAAATTTGCTGACTTCACCTTTTGCACACTGGCAAAATATTTGGACACATGCTCAAAA 1147
DB 421 CCAGAAATTTGCTGACTTCACCTTTTGCACACTGGCAAAATATTTGGACACATGCTCAAAA 480

QY 1148 TTAAGGGAGACATAGATTCAATGAGCTATTGATCTTTAGCAACAAGCTTCATTAGCA 1207

Db

481 TAACAGGGAGACATAGATTCAAAATGAGCTATGGATCTTTAGCAACAAGCTTCATTAGCA 540

QY

1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTACAGTGGGACTGCTTGTATTGAA 1267

Db

541 TTCTTACAAAAGCATTTAGGACTTCATAAAGA-TTGTACAGTGGGACTGCTTGTATTGAA 598

QY

1268 GG-AGATGATGAGATCTTATTCCAGGGACCAACATTAACACA 1309

Db

599 GGCAGATGATGAGAATCTTATTCCAGGGACCAACTATTAAAGCA 641

RESULT

AI343491/c

LOCUS

DEFINITION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI343491 650 bp mRNA EST 08-APR-1999
tb97c04.x1 NCICGAP.Col6 Homo sapiens cDNA clone IMAGE:2062278 3'
similar to SW:PAPA.HUMAN Q13093 PLATELET-ACTIVATING FACTOR
ACETYLHYDROLASE PRECURSOR ;, mRNA sequence.
AI343491 GI:4080697
AI343491.1
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 650)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 785 Std Error: 0.00
Seq primer: -400P from Glnco
High quality sequence stop: 439.

FEATURES

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/tissue_type="colon tumor, RER+"
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP.Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT

ORIGIN

Query Match 42.0%; Score 571.2; DB 10; Length 650;
Best Local Similarity 98.7%; Pred. No. 1.8e-132;
Matches 607; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY 751 CATTGTATCGAAAGCCAGCTGAA--CAATGCTATTAGATTTTAAA-GTTTGTATATGAA-C 806
DB 645 CATTGTATCGAAAGCCAGCTGAAAGAAATGCTTTAGATTTTAAAGTTTATATGGAACC 586

QY 807 AACTGAAGGACTCTATTGATAGGGAAAAAATAGCAGTAATTTGGACATTTCTTTTGGTGGAG 866

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Db 585 ANCTGAAGGACTCTATTATCATAGGGAATAATAGCAGTAATTTGGACATTTCTTTGGTGGAG 526
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Qy 1107 TCACCTTTGCAACTGGCAAAATAATTTGGACACATGCTCAAAATTAAGGGAGACATAGATT 1166
Db 285 TCACCTTTGCAACTGGCAAAATAATTTGGACACATGCTCAAAATTAAGGGAGACATAGATT 226
Qy 1167 CAATCGAGCTATTGATCTTAGCAACAAAGCTTCATTTAGCATCTTACAAAAGCATTTAG 1226
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Qy 1287 TTCAGGGACCAACATTAACAAACCAATCAACATCATGTTACAGAACTCTTCAGGAA 1346
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Qy 1347 TAGAGAAATACAATT 1361
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RESULT 10
Bi182205
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DEFINITION
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UNL-P-FN-bf-g-02-0-UNL 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 874)
Caetano,A.R., Johnson,R.K. and Pomp,D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
Unpublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
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/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
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FEATURES
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library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996.
TAG_SEQ=None found"
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Best Local Similarity 85.7%; Pred. No. 4.6e-122;
Matches 624; Conservative 0; Mismatches 99; Indels 5; Gaps 3;

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Qy 204 TCCCGCGGGGAAATGGGCGCTTATTCGGTGGTGTGACAGACTTAAGTTTGTATCACA 263
Db 112 TCCCGCAGAGAAATGGATCGTACTCGTGGTGTGACCGATCTGATGTTTGTATCACA 171
Qy 264 ATAAGGCACCTTCCTGGCTTATATTCATCCCAAGATATATGCGCTTCGACACC 323
Db 172 AGAAGGCACCTTCCTGGCTTATATTCGTCGCAAGATGTTGACCTTCGACACC 231
Qy 324 TTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAGCAAAATTTCTTGGAAACACAC 383
Db 232 TCTGGATCCCAAGACAAAGAGTATTTTGGGGTCTTAGTAATTTCTCGGAACACAC 291
Qy 384 TTATGGGCAACATTTTGGAGTTACTCTTTGGTTCATGACAACTCTCTGCAAACTGGA 443
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Qy 444 CCCCTCTGAGGCTGCTGAAAAATATCCACTTGTCTTTTCTCATGCTCTGGGCGAT 503
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Qy 564 CTGTAGAACACAGAGATAGATCTGCATCTGCAACTTACATTTTCAAGGACCAATCTG 623
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Qy 801 TGGAAACAACTCAAGCACTCTATTGATAGGAAAAAATAGCAAGTAATTTGACATTTCT 860
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Db 140 TTGCTTGAAGGAGATGATGAGATCTTTATTCAGGAGCCAAACATTAACACAAACCAATCAA 81
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LOCUS 602919996F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5060590 5'
DEFINITION mRNA sequence.
ACCESSION BI159467
VERSION BI159467
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1163 row: 0 column: 23
High quality sequence stop: 791.
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
for transgenic model: Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NIH_CGAP Library."
BASE COUNT 200 a 201 c 191 g 225 t
ORIGIN

Query Match 32.1%; Score 436.4; DB 11; Length 817;
Best Local Similarity 75.7%; Pred. No. 9.8e-99;
Matches 581; Conservative 0; Mismatches 181; Indels 6; Gaps 3;

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QY 65 TTCTGCTCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
Db 112 TTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 171
QY 125 GTTGCCCATATGAATCATCAGCATGGTCAACAAATTAACAAAGTACTGCTGCTGCTGCT 184
Db 172 TTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
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QY 305 AATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAGCAAA 364
Db 349 CAAGTCCGCTCGACACTGTTTGGATCCCAACAAGAATATATTTTGGGCTCTTAGTATA 408
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ACCESSION BG918925
VERSION BG918925.1 GI:14299401
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10899 row: 1 column: 11
High quality sequence stop: 756.
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Job time: 4547 sec

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 Percent Similarity: 100.000 Percent Identity: 100.000

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1088 CACCAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
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401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuII 417
1288 TCCAGGACCAACATTAACACACCAACCAATCAACATCATGTTTACAGAACT 1337
417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
1338 CTTCAGGAATAGAGAAATACAAT 1360
434 erSerGlyIleGluLysTyrAsn 441

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seq_name: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT: AAR64928

seq_documentation_block:

ID AAR64928 standard; Protein; 442 AA.

XX AAR64928;

DT 18-AUG-1995 (first entry)

DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.

KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;

KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 25..31 "Peptide 4"

FT Peptide /note= "Peptide 4"

FT Peptide 115..133

FT Peptide /note= "Peptide 3"

FT Peptide 298..327

FT Peptide /note= "Peptide 2"

FT Peptide 368..393

FT Peptide /note= "Peptide 1"

XX

1338 CTTGAGGAATAGAGAAATACAAAT 1360

|||||
434 erSerGlyIleGluLysTyrAsn 441

seq_name: /SDS2/gcgdata/geneseq/geneseq/AA1995.DAT: AAR71913

seq_documentation_block:

ID AAR71913 standard; Protein; 441 AA.

XX AC AAR71913;

XX DT 05-DEC-1995 (first entry)

XX DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX PN W09509921-A.

XX PD 13-APR-1995.

XX PF 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX DR N-PSDB; AAQ87947.

XX PT New nucleic acid encoding platelet activating factor,
XX PT acetyl:hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy

XX PS Claim 5; Page 53-54; 88pp; English.

XX CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
XX CC is useful in the treatment of inflammatory diseases, in particular
XX CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
XX CC raising monoclonal antibodies specific for PAF-AH that are useful in
XX CC the diagnosis of such diseases.

XX SQ Sequence 441 AA;

alignment_scores:

Quality: 2354.00 Length: 441
Ratio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAR71913 ..

Align seg 1/1 to: AAR71913 from: 1 to: 441

38 ATGTGCGCCACCACAAATTCATGCTGCTTTCTGCCTCTGGGCGTCGCCGCGC 87

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1 MetValProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17

88 TGTGTTTATCTTTTGTACTGCGCAATACATAAATCTGTTGCCCATATGA 137

|||||
17 aValValTyrProPheAspTyrPGLnTyrIleAsnProValAlaHisMetL 34

138 AATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCTGCAAGC 187

|||||

34 ysSerSerAlaTrrpValAsnLysIleGlnValLeuMetAlaAlaSer 50
188 TTTTGGCCAAACTAAATCCCCGGGGAATGGCCCTTATTCCTGTTGGTTG 237
|||||
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
238 TACAGACTTAATGTTTGTATCAGCTAATAAGGGCACCTCTCTTCGCTTAT 287
|||||
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84
288 ATTATCCATCCCAAGATAATGATCGCCTTGACACCCCTTTGGATCCCAAT 337
|||||
84 yrTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrrpIleProAsn 100
338 AAAGAATAATTTTGGGCTCTTAGCAAAATTTCTTGGAACACACATGGCTTAT 387
|||||
101 LysGluTyrPheTrrpGlyLeuSerLysPheLeuGlyThrHisTrrpLeuMe 117
388 GGGCAACATTTTGGAGTTTACTCTTTTGGTTCATGACAACTCCTGCAACT 437
|||||
117 tGlyAsnIleLeuArgLeuPheGlySerMetThrThrProAlaAsnT 134
438 GGAATTCCTCTCTCAGGCTGGTGAATAATATCCACTTGTGTTTTTCT 487
|||||
134 rPasnSerProLeuArgProGlyGluLysTyrProLeuValValPheSer 150
488 CATGGCTCTTGGGCGATTTCAGGACACTTTTATTTCTGCTATTGGCATGACCT 537
|||||
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyLeAspLe 167
538 GGCACTTCATGCTGGTGTATAGTTGCTGTAGTGTAGAACACACAGATAGATCTG 587
|||||
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSera 184
588 CATCTGCAACTTACTATTTCAGGACCACTCTGTCGACAAATAGAGGAC 637
184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyLeAsp 200
638 AACTCTTGGCTCTACCTTAGAACCTGAAACAGAGAGGAGGACACATAT 687
|||||
201 LysSerTrrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217
688 ACGAAATAGCAGGTACGCGCAAGACGAAAAAGAAATGTTCCCAAGCTCTCA 737
|||||
217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeu 234
738 GTCTGATTCTTGGACATTGATCATGGAAGCCAGTGAAGAAATGCATTAGAT 787
234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
788 TTAAGTCTTTCATATGGAACAACATGAAGGACTCTATTGATAGGAAAAAT 837
|||||
251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysI 267
838 AGCAGTAATTGGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTA 887
|||||
267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeu 284
888 GTGAAGATCAGAGATTTCAGATGTTGTTATTCCTGCTGATGATGATGTTT 937
|||||
284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrrpMetPhe 300
938 CCACCTGGGTGATGAAGTATATATCCAGAAATTCCTCAGCCCTCTCTTTTAT 987
|||||
301 ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheI 317
988 CAACCTCTGAATATTTCCATATCTGCTTAATATCATATAAATGAAAAAT 1037
|||||
317 eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
1038 GCTACTCAGCTGATAAAGAAAGAAAGATGATTACAAATCAGGGTTCAGTC 1087
334 ystySerProAspLysGluArgLysMetIleThrIleArgglySerVal 350

1088 CACCAGAAATTTGCTGACTTCACCTTTGCAACTGGCAAAATAATGAGACA 1137
 351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHI 367
 1138 CATGCTCAAAATTAAGGAGACATAGATTCAAAATGACGCTATTGATCTTA 1187
 367 sMetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384
 1188 GCAACAAAGCTTCATTAGCATTCCTTACAAAAGCATTTAGGACTTCATATA 1237
 384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
 1238 GATTGTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAATCTTAT 1287
 401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuI 417
 1288 TCCAGGGACCAACATTAACACAAACCAATCAACACATCATGTTACAGAACT 1337
 417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
 1338 CTTACGGAATAGAGAAATACAAAT 1360
 434 erSerGlyIleGluLysTyrAsn 441

seq_name: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT:AAW26498

seq_documentation_block:

ID AAW26498 standard; Protein: 441 AA.

XX AC AAW26498;

XX DT 05-JAN-1998 (first entry)

XX DE Human platelet-activating factor acetylhydrolase.

XX KW Platelet-activating factor acetylhydrolase; PAF-AH; human;
 inflammation; asthma; pleurisy; necrotising enterocolitis;
 adult respiratory distress syndrome; therapy.

XX OS Homo sapiens.

XX PN US5656431-A.

XX PD 12-AUG-1997.

XX PF 06-OCT-1993; 93US-0133803.

XX PR 07-JUN-1995; 95US-0483232.

XX PR 06-OCT-1993; 93US-0133803.

XX PR 06-OCT-1994; 94US-0318905.

XX PA (ICOS) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX PI Wilder CL;

XX DR WPT; 1997-414580/38.

XX DR N-PSDB; AAT87048.

XX PT Detecting lesions in human platelet-activating factor
 acetylhydrolase gene - by comparison with defined wild-type gene
 sequence

XX PS Example 3; Column 47-50; 53pp; English.

XX CC This polypeptide comprises human plasma platelet-activating factor
 acetylhydrolase (PAF-AH), a protein that inactivates PAF and
 inactivates oxidatively fragmented phospholipids such as products of
 the arachidonic acid cascade that mediate inflammation. Its
 sequence was deduced from a full-length cDNA clone (see AAT87048)
 obtained from a macrophage cDNA library. Mouse, dog, cattle,
 chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have

CC also been identified. Recombinant PAF-AH polypeptides can be
 produced in prokaryotic or eukaryotic host cells and used to mimic
 or augment normal processes of resolution of inflammation in vivo.
 CC Examples describe the in vivo therapeutic effect of recombinant
 PAF-AH products on acute inflammation, pleurisy, asthma,
 CC necrotising enterocolitis and adult respiratory distress syndrome
 CC in animal models.

XX SQ Sequence 441 AA;

alignment_scores: Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAW26498 ..

Align seg 1/1 to: AAW26498 from: 1 to: 441

38 ATGGTGCACCCCAAAATGTCATGTGCTTTCTGCTCTGCGCTGCCCTGGC 87
 1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17
 88 TGTGGTTTATCCTTTTGACTGGCAATACATAAATCCTGTTGCCCATATGA 137
 17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
 138 AATCATCAGCATGGTCAACAAATAACAAGTACTGATGGCTGCTGCAAGC 187
 34 ySerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaLaser 50
 188 TTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTGGTGGT 237
 51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
 238 TACAGACTTATGTTGATCACACTAATAAGGGACCTTCTTGGCTTTAT 287
 67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84
 288 ATTATCCATCCCAAGATAATGATCGCTTGCACCTTTGGATCCCAAT 337
 84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProasn 100
 338 AAGATATATTTTGGGGTCTTTAGCAAAATTTCTTGGACACACTGGCTTAT 387
 101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
 388 GGGCAACATTTTGAGGTACTCTTTGGTTCATGACAACTCCTGCAAACT 437
 117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134
 438 GGAATCCCTCTGAGGCTCGTGAATAATATCCACTTGTGTTTCTTCT 487
 134 rPAsnSerProLeuArgProGlyGluLysTyrProLeuValValPheSer 150
 488 CATGGTCTTGGGGCATTCAGGACACTTTTATTCTGCTATTGGCACTGACCT 537
 151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
 538 GGCATCTCATGGTTTATAGTGTGCTGCTAGACACAGAGATAGTCTG 587
 167 uAlaSerHisGlyPheIleValAlaValGluHisArgAspArgSerA 184
 588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAAGAAATAGGGAC 637
 184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaIleGlyAsp 200
 638 AAGTCTTGGCTCTACCTTAGAACCTTGAACAAAGAGGAGGAGACATAT 687
 201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217

```

688  ACGAATGAGCAGGTATCGGCAAGCAAGAAAGATGTTCCCAAGCTCTCA 737
      |||
217  eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234
      |||
738  GTCGATCTTGCAGATTCATGGAAGCCAGTCGAGGAATGATAGAT 787
      |||
234  erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
      |||
788  TTAAGTTTGCATATGGCAACTGAGGCACTCTATTGATAGGGAATAAT 837
      |||
251  LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysII 267
      |||
838  AGCAGTAATTCGACATCTTTTGGTGGCAACGCTTATTTCAGACTCTTA 887
      |||
267  eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284
      |||
888  GTGAAGATCAGAGATTCAGATTCGATTCGCTGGATGCGATGATGTTT 937
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284  erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
      |||
938  CCAGTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCCCTCTTTTAT 987
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301  ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheII 317
      |||
988  CAACTCTGAATATTCGAATATCTCTGCTAATATCATATAAAATGAAAAAT 1037
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317  eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
      |||
1038  GCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGTTCAGTC 1087
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334  ystYrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350
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1088  CACCAGAAATTTGCTGACTTTCACCTTTTGCACACTGGCAAAATAATTGGACA 1137
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351  HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHI 367
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1138  CATGCTCAATTAAGGACACATAGATTCAATGCAGCTATTGATCTTA 1187
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367  smetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384
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1188  GCAACAAGCTTCATTAGCATCTTACAAAGCATTTAGGACTTCATAAA 1237
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384  erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
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1238  GATTTTGATCAGTGGACCTGCTGATTGAAGGAGATGATGAGAATCTTAT 1287
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401  AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuII 417
      |||
1288  TCCAGGACCAACATTAAACACACCAATCAACACATCATGTTACAGAACT 1337
      |||
417  eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
      |||
1338  CTTCAAGATAGAGAATAACAAT 1360
      |||
434  erSerGlyIleGluLysTyrAsn 441

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seq_name: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.AAW23796

seq_documentation_block:

ID AAW23796 standard; protein; 441 AA.

XX AC AAW23796;

XX DT 04-NOV-1997 (first entry)

XX DE Human plasma platelet activating factor acetylhydrolase.

XX KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
 KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
 KW central nervous system shock; arthritis; Crohn's disease;
 KW systemic lupus erythematosus; adult respiratory distress syndrome.
 XX OS Homo sapiens.

```

XX PN US5641669-A.
XX PD 24-JUN-1997.
XX PF 06-OCT-1993; 93US-0133803.
XX PR 06-OCT-1994; 94US-0318905.
XX PR 06-OCT-1993; 93US-0133803.
XX PA (ICOS-) ICOS CORP.
XX PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
XX PI Wilder CL;
XX DR WPI; 1997-340947/31.
XX DR N-PSDB; AAT80564.
XX PT New human plasma platelet activating factor acetylhydrolase -
XX PT useful as anti-inflammatory for treatment of asthma, anaphylaxis,
XX PT shock, etc
XX PS Claim 1; Column 35-38; 43pp; English.
XX CC The present sequence represents the purified and isolated human plasma
XX CC platelet activating factor acetylhydrolase (PAF-AH). This novel
XX CC polypeptide inactivates PAF and oxidatively fragmented phospholipids
XX CC such as pro-inflammatory arachidonic acid metabolites, and so can be
XX CC used to treat inflammation by augmenting endogenous activity. Typical
XX CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
XX CC central nervous system shock, arthritis, Crohn's disease, systemic
XX CC lupus erythematosus, adult respiratory distress syndrome. The
XX CC polypeptide can also be used to raise specific antibodies (Ab) which
XX CC are useful as immunoassay reagents and for generating anti-idiotypic
XX CC antibodies. The nucleic acid encoding the protein can be used to screen
XX CC for related genes; in hybridisation assays to assess the protein-
XX CC producing cells; to generate knockout mice; to detect genetic mutations
XX CC and (antisense sequences) to inhibit the protein expression. Unlike PAF
XX CC receptor antagonists, the protein is a natural component of plasma.
XX SQ Sequence 441 AA;

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alignment_scores:

Quality: 2354.00 Length: 441
 Ratio: 5.328 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAW23796 ..

Align seg 1/1 to: AAW23796 from: 1 to: 441

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1  MetValProProlLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17
      |||
88  TGTGGTTTATCCCTTTGACTGGCAATACATAAATCCTGTTGCCCATATGA 137
      |||
17  aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
      |||
138  AATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGCTGCAAGC 187
      |||
34  ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaLaser 50
      |||
188  TTTGGCCAAACTAAATCCCGGGGAAATGGGCCTTATTCCTGTTGGTTG 237
      |||
51  PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
      |||
238  TACAGACTTAATGTTTGATCACACTAATAAGGCACCTCTCTGGCTTAT 287
      |||
67  sthrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84

```



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288 ATTATCCATCCCAAGATAAATGATCGCCTTGACACCCCTTTGGATCCCAAT 337
84 yTYrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100
338 AAAGAATATTTTGGGTCTTAGCAAAATTTCTTGAACACACTGGCTTAT 387
101 LysGluTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
388 GGGCAACATTTTGGAGTACTCTTTGGTTCAATGACAACACTCTGCAAACT 437
117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134
438 GGAATCCCTCTGAGCCTCGTGAATAATATCCACTTCTGTTTCTTCT 487
134 rPasnSerProLeuArgProGlyGluTyrProLeuValValPheSer 150
488 CATGGCTCTGGGCATTGAGACACTTTTATTCTGCTATTGGCACTGACCT 537
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
538 GGCATCTAGGGTTTATAGTTGCTGCTGTAGAACACACAGATAGATCTG 587
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSerA 184
588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGAC 637
184 laSerAlaThrTyrTyrPheLysaspGlnSerAlaAlaGluIleGlyAsp 200
638 AAGTCTTGGCTCTACCTTAGAACCTGAAACAAAGAGGAGGAGACACATAT 687
201 LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisI 217
688 ACGAAATGAGCAGGTACGGCAAGACAAAGAAAGATGTTCCCAAGCTCTCA 737
217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234
738 GTCTGATCTTGACATTCATCATGGAAGCCAGTGAAGAAATCATTAGAT 787
234 eLeuIleLeuAspIleaspHisGlyLysProValLysAsnAlaLeuasp 250
788 TTAAGTTTGTATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAAT 837
251 LeuLysPheaspMetGluGlnLeuLysaspSerIleAspArgGluLysI 267
838 AGCAGTAAATGGCACTCTTTTGGTGGGACACGCTTATTCAGACTCTTA 887
267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284
888 GTGAAGATCAGAGATTCAGATGCTGCTATTGCCCTGATGCATGGATGTTT 937
284 eGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
938 CCAGTGGTGTATGAAGTATATTCAGAATTCCTCAGCCCTCTTTTAT 987
301 ProLeuGlyaspGluValTyrSerArgIleProGlnProLeuPhePheI 317
988 CAACCTCGAATATTTCCCAATATCCTGCTTAATATATCAATAAAGCAAAAT 1037
317 eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
1038 GCTACTCACCTGATAAGAAAGAAAGATGATTACAAATCAGGGGTTTCAGTC 1087
334 yTYrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350
1088 CACCAGAAATTTTGTGACTTCACTTTTGGAACTGGCAAAATATATGGACA 1137
351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHi 367
1138 CATGCTCAATTAAGGGACATGATTCAAATGCAGCTATTGATCTTA 1187
367 sMetLeuLysLeuLysGlyAspIleaspSerAsnValAlaIleaspLeuS 384
1188 GCAACAAAGCTTCATTAGCATTTCTTACAAAGCATTTTAGGACTTCATAA 1237

```

```

|||||
384 erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
1238 GATTTTGATCAGTGGGACTGCTTGAAGGAGATGATGAGAACTCTAT 1287
|||||
401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuI 417
1288 TCCAGGGACCAACATTAAACAAACCAATCAACACATCATGTTACAGAACT 1337
417 eProGlyThrAsnIleAsnThrAsnGlnHisIleMetLeuGlnAsnS 434
1338 CTTCAGGAATAGAGAAATACAAT 1360
434 erSerGlyIleGluLysTyrAsn 441
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seq_name: /SIDS2/gcdata/geneseq/geneseq/AA1997.DAT:AAW09808
seq_documentation_block:
ID AAW09808 standard; Protein; 441 AA.
XX
AC AAW09808:
XX
DT 12-JUN-1997 (first entry)
XX
DE Platelet-activating factor acetylhydrolase.
XX
KW Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
KW mutation; V279F; substitution; restriction fragment length polymorphism;
KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
KW asthmatic children; treat; inflammatory condition.
XX
OS Homo sapiens.
XX
FH Peptide
FT 1..41
FT /label= signal_peptide
FT /note= "possibly contains additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT
FT Protein
FT 42..441
FT /label= mature_enzyme
FT
FT Active-site
FT 271..275
FT /note= "contains active site serine; conforms to
FT consensus motif for mammalian and microbial
FT lipases and serine proteases"
XX
PN US5605801-A.
XX
PD 25-FEB-1997.
XX
PF 06-OCT-1993; 93US-0133803.
XX
PR 06-OCT-1994; 94US-0318905.
PR 06-OCT-1993; 93US-0133803.
PR 07-JUN-1995; 95US-0478465.
XX
PA (ICOS-) ICOS CORP.
XX
PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
PI Wilder CL;
XX
XX WPI; 1997-153573/14.
XX N-PSDB; AAT63701.
XX
XX Detection of platelet-activating factor acetylhydrolase gene
XX mutation - by restriction length polymorphism analysis
XX
XX Example 3; Column 33-38; 43pp; English.
XX
XX This sequence is that of human platelet-activating factor acetyl-
XX hydrolase (PAF-AH).
XX The claimed method of the invention detects a mutation (which results
XX in a V279F substitution) in the PAF-AH gene, and comprises performing a
XX restriction fragment length polymorphism analysis and differentiating

```

CC between wild-type and mutant alleles on the basis of the number of
 CC restriction sites. The method is useful for diagnosis of inherited PAF-AH
 CC deficiency, which has been correlated with severe respiratory symptoms in
 CC asthmatic children. Recombinant PAF-AH can be used to treat inflammatory
 CC conditions.

XX
 SO Sequence 441 AA;

alignment_scores:

Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAW09808 ..

Align seg 1/1 to: AAW09808 from: 1 to: 441

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38 ATGGTGCCACCACAAATTCATGCTGCTTTCTGCTCTGCGCTGCGCTGC 87
|||||
1 MetValProProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17

88 TGTGCTTTATCCTTTTGACTGCAATACATAATCTCTGTGCCCATTGA 137
|||||
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34

138 AATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCGCAAGC 187
|||||
34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50

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ID AAW38361 standard; Protein; 441 AA.
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XX AC AAW38361;
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XX DT 31-MAR-1998 (first entry)
XX
XX DE Human plasma platelet activating factor acetylhydrolase.
XX
XX KW Human; plasma platelet activating factor acetylhydrolase;
XX KW monoclonal antibody; immunoassay; diagnosis; asthma;
XX KW detection.
XX
XX OS Homo sapiens.
XX
XX PN US5698403-A.
XX

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PD 16-DEC-1997.
 XX 07-JUN-1995; 95US-0483140.
 XX 06-OCT-1994; 94US-0318905.
 PR 06-OCT-1993; 93US-0133803.
 PR 07-JUN-1995; 95US-0483140.
 XX
 PA (ICOS-) ICOS CORP.
 XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
 PI Wilder CL;
 XX
 DR WPI; 1998-051484/05.
 DR N-PSDB; AAT96127.
 XX
 PT - useful for platelet activating factor acetylhydrolase, PAF-AH
 PT - useful to diagnose disorders associated with abnormal PAF-AH level
 XX
 PS Claim 1; Columns 35-38; 47pp; English.
 XX
 CC The present sequence was used in the development of a method for
 CC detecting human, mouse, canine, rat and monkey plasma platelet
 CC activating factor acetylhydrolases (PAF-AH). The method comprises
 CC contacting serum with PAF-AH specific monoclonal antibody (Mab) to
 CC form a PAF-AH/Mab complex, and detecting the complex. The method
 CC can be used to diagnose disorders associated with abnormal PAF-AH
 CC levels, and to monitor therapy of such disorders. Plasma PAF-AH
 CC deficiency has been correlated with severe respiratory symptoms in
 CC asthmatic children who appear to have inherited the deficiency in
 CC an autosomal recessive manner.
 XX
 SQ Sequence 441 AA;

alignment_scores:
 Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

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 138 AATCATCAGATGGGTCAACAAATACAGTACTGATGGCTGCTGCAAGC 187
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seq_documentation_block:

ID AAW96334 standard; Protein; 441 AA.

AC AAW96334;

DT 28-JUN-1999 (first entry)

DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).

XX Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;
KW platelet activating factor; inflammation; treatment; hydrolysis;
KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;
KW acute respiratory distress syndrome; pancreatitis;
KW neurological disease; HIV; human immunodeficiency virus.

XX Homo sapiens.

XX WO9909147-A1.

XX 25-FEB-1999.

XX 13-AUG-1997; 97WO-US14212.

XX 13-AUG-1997; 97WO-US14212.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
PI Wilder CL;

XX WPI; 1999-181028/15.
DR N-PSDB; AAX08463.

XX New truncated human platelet-activating factor acetylhydrolase and
PT its encoding polynucleotides - useful for regulating inflammatory
PT events

XX Claim 1; Page 97-98; 136pp; English.

XX Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be
CC used to inactivate the pathological effects of PAF.
CC Pathological conditions which can be treated include pleurisy,
CC asthma, rhinitis, necrotizing enterocolitis, acute respiratory
CC distress syndrome, acute pancreatitis or neurological disease
CC associated with HIV infection. Identification and isolation of
CC polynucleotide sequences encoding human plasma PAF-AH allows the
CC recombinant production of PAF-AH. This makes possible the use of
CC exogenous PAF-AH to mimic or augment normal processes of resolution
CC of inflammation in vivo. PAF inactivation occurs by hydrolysis of
CC the PAF sn-2 acetyl group by PAF-AH. PAF-AH also metabolises
CC oxidatively fragmented phospholipids such as products of the
CC arachidonic acid cascade which mediate inflammation. Administration
CC of PAF-AH is advantageous to administering PAF receptor antagonists
CC since PAF-AH is a product normally found in plasma. Because PAF
CC receptor antagonists are structurally related to PAF they
CC competitively inhibit native PAF-AH activity. Treatment with
CC recombinant PAF-AH would augment endogenous PAF-AH activity and
CC compensate for any inactivated endogenous enzyme.

XX Sequence 441 AA;

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Quality: 2354.00

Length: 441

Ratio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.773

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XX AC AAW73359;

XX DT 12-FEB-1999 (first entry)

XX DE Human PAF-AH protein sequence.

XX OS Homo sapiens.

XX PN US5847088-A.

XX PD 08-DEC-1998.

XX PF 07-JUN-1995; 95US-0485938.

XX PR 07-JUN-1995; 95US-0485938.

XX PR 06-OCT-1993; 93US-0133803.

XX PR 06-OCT-1994; 94US-0318905.

XX PA (ICOS-) ICOS CORP.

XX PI Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

XX PI Wilder CL;

XX XX

DR WPI: 1999-059148/05.
 DR N-PSDB; AAV08534.
 XX
 PT Antibodies specific for platelet-activating factor acetylhydrolase
 PT proteins - useful for detecting or purifying the proteins
 XX
 PS Claim 1: Column 45-48; 59pp; English.
 XX
 CC This sequence represents the human platelet-activating factor
 CC acetylhydrolase (PAF-AH). This protein is specifically bound by
 CC the antibody of the invention. The monoclonal antibody of the invention
 CC is useful for detecting or purifying PAF-AH proteins.
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 Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
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seq_name: /SIDS2/ycgdata/geneseq/geneseq/AA2000.DAT: AAB07774

seq_documentation_block:

ID AAB07774 standard; Protein: 441 AA.

XX AC AAB07774;

XX DT 14-NOV-2000 (first entry)

XX DE Plasma platelet-activating factor acetylhydrolase.

XX KW Platelet-activating factor acetylhydrolase; platelet-activating factor;

reperfusion injury; acute inflammation; pleurisy; asthma;
necrotising enterocolitis; adult respiratory distress syndrome.
Homo sapiens.
US6099836-A.
08-AUG-2000.
19-JUN-1998; 98US-0100546.
07-JUN-1995; 95US-0480658.
22-JAN-1998; 98US-0010715.
06-OCT-1993; 93US-0133803.
06-OCT-1994; 94US-0318905.
(ICOS-) ICOS CORP.
Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;
Cousens LS;
WPI: 2000-531654/48.
N-PSDB; AAA59579.
Treating mammal susceptible to or suffering from platelet-activating
factor mediated condition associated with reperfusion injury such as
acute inflammation, pleurisy, asthma, necrotising enterocolitis -
Example 3; Column 49-52; 55pp; English.
The specification describes a pharmaceutical composition comprising
platelet-activating factor acetylhydrolase. The composition is
administered for treating a mammal susceptible to or suffering from
a platelet-activating factor-mediated condition associated with
reperfusion injury. Diseases and conditions which may be treated
include acute inflammation, pleurisy, asthma, necrotising enterocolitis
and adult respiratory distress syndrome. The present sequence represents
human plasma platelet-activating factor acetylhydrolase.
Sequence 441 AA;

alignment_scores:

Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAB07774 ..

Align seg 1/1 to: AAB07774 from: 1 to: 441

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1 MetValProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17
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88 TGTGTTTATCTTTTCTGCTGCAATACATAAATCTCTGCTCCCATATGA 137
|||||
17 aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
|||||
138 AATCATCAGCATGGGTCAACAAACAAATACAGTACTGATGGCTGCTGCAAGC 187
|||||
34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaAlaSer 50
|||||
188 TTTGGCCAAACTAAATCCCGGGGAAATGGGCCTTATTCCTGGTTGTTG 237
|||||
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
|||||
238 TACAGACTTAATGTTTGTATCACACTAATAAGGACACCTCTCTTGGCTTAT 287
|||||
67 sthrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84
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288 ATTATCCATCCCAAGATAATGATCGCTTGCACACCCCTTTGGATCCCAAT 337
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84 yrTyProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100
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338 AAAGAATAATTTTGGGGCTTACCAAAATTTCTTGGAAACACACATGGCTTAT 387
|||||
101 LysGluTyProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 117
|||||
388 GGGCAACATTTTGGAGTTACTCTTTGGTTCAATGACAACTCTCGCAAACT 437
|||||
117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134
|||||
438 GGAATTCCTCTGAGGCTGTGTAATAATATCCACTTGTGTTTCTTCT 487
|||||
134 rPAsnSerProLeuArgProGlyGluLysTyProLeuValPheSer 150
|||||
488 CATGCTCTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTTGACCT 537
|||||
151 HisGlyLeuGlyAlaPheArgThrLeuTySerAlaIleGlyLeuAspLe 167
|||||
538 GGCATCTCATGGTTTATAGTTGCTGCTAGAACACACAGATAGATCTG 587
|||||
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSera 184
|||||
588 CATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637
|||||
184 LaSerAlaThrTyTrpPheLysAspGlnSerAlaAlaGluIleGlyAsp 200
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638 AAGCTCTGCTCTACCTTAGAACCTTGAACCAAGAGAGAGAGACACATAT 687
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201 LysSerTrpLeuTyLeuArgThrLeuLysGlnGluGluThrHisIle 217
|||||
688 ACRAAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCA 737
|||||
217 eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234
|||||
738 GTCGTATCTTGACATGTATCATGTGGAAGCCAGTGAAGATGCAATAGAT 787
|||||
234 erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
|||||
788 TTAAGTTGTATATGAACAACCTGAGGACTCTATTGATAGGGAANAAT 837
|||||
251 LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysIle 267
|||||
838 AGCAGTAATTTGACATCTCTTTGGTGGAGCAACGGTTATTCAGACTCTTA 887
|||||
267 eAlaValIleGlyHisSerPheGlyAlaThrValIleGlnThrLeuS 284
|||||
888 GTGAAGATCAGAGATTCAGATGTGTTGCTGCTGATGATGATGATGTTT 937
|||||
284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
|||||
938 CCACTGGGTGATGAGTATATTTCCAGAAATCTCTCAGCCCTCTTTTAT 987
|||||
301 ProLeuGlyAspGluValTySerArgIleProGlnProLeuPheIle 317
|||||
988 CAACCTCAATATTTCCCAATCTCTCTAATATCATATAAAATGAAAAAT 1037
|||||
317 eAsnSerGluTyPheGlnTyProAlaAsnIleIleLysMetLysLysC 334
|||||
1038 GCTACTCACCTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 1087
|||||
334 yTySerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350
|||||
1088 CACCAAGATTTTGGCTGACTTCACTTTGCACTGGCAAAATAATATGGA 1137
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351 HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHi 367
|||||
1138 CATGCTCAATTAAGGGAGACATGATTCAAATGCAGCTATTGATCTTA 1187
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367 sMetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384
|||||
1188 GCAACAAAGCTTCATAGCATCTTACAAAAGCATTTTAGGACTTCATAAA 1237
|||||

384 eAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
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1238 GATTTTGATCAGTGGGACTGCTTATTGATGAAGGAGATGATGAGAATCTTAT 1287
|||||
401 AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuIle 417
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1288 TCCAGGGACCAACATTAAACACCAATCAACACATCATGTTTACAGAACT 1337
|||||
417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
|||||
1338 CTTCAAGGAATAGAGAAATACAAT 1360
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434 eSerGlyIleGluLysTyAsn 441
seq_name: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:AAV88301
seq_documentation_block:
ID: AAY88301 standard; Protein; 441 AA.
XX AC AAY88301;
XX DT
XX DT 14-JUL-2000 (first entry)
XX DE Human platelet-activating factor acetyl hydrolase amino acid sequence.
XX KW Platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;
KW inflammatory response; pre-term labour; pharmaceutical composition;
KW regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease;
KW pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.
XX KW
XX OS Homo sapiens.
XX PN US6045794-A.
XX PD 04-APR-2000.
XX XX 09-JUN-1999; 99US-0328474.
XX PR 12-AUG-1997; 97US-0910041.
XX PR 06-OCT-1993; 93US-0133803.
XX PR 06-OCT-1994; 94US-0318905.
XX PR 07-JUN-1995; 95US-0483232.
XX PA (ICOS-) ICOS CORP.
XX PI Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
PI Eberhardt CD;
XX DR WPI; 2000-282671/24.
XX DR N-PSDB; AAA10861.
XX PT Treatment of mammals suffering from pre-term labour comprises
PT administering a pharmaceutical composition comprising
PT platelet-activating factor acetyl hydrolase enzyme -
XX PS Claim 1; Column 67-70; 67pp; English.
XX CC This sequence represents the human platelet-activating factor acetyl
CC hydrolase (PAF-AH) amino acid sequence. PAF is a phospholipid and is
CC implicated in pathological inflammatory responses (e.g. asthma,
CC anaphylaxis, septic shock and arthritis). PAF-AH is released by
CC hepatocytes, and macrophages and inactivates PAF. PAF-AH also inactivates
CC oxidatively fragmented phospholipids that mediate inflammation. This
CC sequence is specifically claimed for use in a method to treat a mammal
CC suffering from pre-term labour. PAF-AH is included in a pharmaceutical
CC composition which can be administered to a mammal suffering from pre-term
CC labour. The invention relates to purified and isolated polynucleotide
CC sequences encoding human PAF-AH and materials and methods for the
CC recombinant production of PAF-AH products which are expected to be useful
CC in regulating inflammatory events. The administration of PAF-AH to
CC animals may be used for ameliorating pathological inflammatory conditions
CC such as asthma, anaphylaxis, shock, arthritis, Crohn's disease,
CC pancreatitis, allergic inflammation, and human immunodeficiency virus

234	erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp	250
788	TTAAAGTTTGCATATGGAACAACATGAAGACTCTATTGCATAGGGAAGAAAAT	837
251	LeuLysPheAspMetGluGlnLeuLysAspSerIleasparGluLysII	267
838	AGCAGTAANTTGGACATCTCTTTGGTGGAGCAAGCGTTATTTCAGACTCTTA	887
267	eAlaValIIeGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS	284
888	GTCAAGATCAGAGATTCAGATGCGTATTCGCCCTGGATGCATGCATGTTT	937
284	erGluAspGlnAtrGpPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe	300
938	CCACTGGGTGATCAAGTATATTCAGAAATTCCTCAGCCCTCTCTTTTAT	987
301	ProLeuGlyAspGluValTySerArgIleProGlnProLeuPhePheII	317
988	CAACTCTGAATATTTCCAATATCTGCTAATATCATATAAATAAGAAAAAT	1037
317	eAsnSerGluTyPheGlnTyPProAlaAsnIleIleLysMetLysLysC	334
1038	GCTACTCACTGATAAGAAAGAAAGATGATTCAATCAGCGGCTTCAGTC	1087
334	ysTySerProAspLysGluArgLysMetIleThrIleArgLysSerVal	350
1088	CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACA	1137
351	HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHI	367
1138	CATGCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGCATCTTA	1187
367	sMetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS	384
1188	GCACAAAGCTTCATTAGCATCTCTTACAAAGCATTTAGACTTCATAAA	1237
384	erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys	400
1238	GATTTTGCATGAGGGACCTGCTTGATTGAAGGAGATGCATCAGAACTCTAT	1287
401	AspPheAspGlnTrpAspCysLeuIIeGluGlyAspAspGluAsnLeuII	417
1288	TCAGGGGACCAACATTTAACACACCAACATCAACACATCATCTTTACAGAACT	1337
417	eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS	434
1338	CTTCAGGAATAGAGAAATCAAT	1360
434	erSerGlyIleGluLysTyraSn	441
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seq_documentation_block:		
ID	AA50735 standard; Protein; 441 AA.	
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AC	AA50735;	
AC		
XX		
DT	08-FEB-2000 (first entry)	
XX		
DE	Human PAF-AH protein.	
XX		
KW	Platelet activating factor acetylhydrolase; PAF-AH; human;	
KW	antiinflammatory; antiasthmatic; antiallergic; antiarthriti	
KW	antichemic; inflammatory disorder; anaphylaxis; ulcerativ	
XX	antigen-induced arthritis; ischemia; septicemia; allergy.	
XX		
OS	Homo sapiens.	
XX		
PN	US5977308-A.	
XX		
PD	02-NOV-1999.	
XX		
XX	12-AUG-1997; 97US-0910041.	

XX 06-OCT-1993; 93US-0133803.
 PR 06-OCT-1994; 94US-0318905.
 PR 07-JUN-1995; 95US-0483232.
 XX (ICOS-) ICOS CORP.
 XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
 PI Eberhardt CD;
 XX WPI; 2000-021956/02.
 DR N-PSDB; AA224240.
 XX Truncated and substituted versions of human platelet activating factor
 PT acetylhydrolase, for treating or preventing inflammatory diseases such
 PT as asthma -
 XX Example 3; Column 63-66; 65pp; English.
 XX This invention describes novel truncated and variant forms (I) of human
 CC PAF-AH (platelet activating factor acetylhydrolase) which have
 CC antiinflammatory, antiallergic, antiallergic, antiarthritic and
 CC antiischemic activity. (I) are used to treat a wide variety of
 CC inflammatory disorders, e.g. asthma, anaphylaxis, antigen-induced
 CC arthritis, ulcerative colitis, ischemia, septicemia, allergy, etc.
 CC Recombinant (I), produced in prokaryotic cells, are less heterogeneous
 CC at the termini than the full-length protein. Some of the truncated
 CC versions also have greater activity than the wild-type enzyme. This
 CC sequence represents the human PAF-AH protein which is described in the
 CC method of the invention.
 XX Sequence 441 AA;

alignment_scores:

Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAY50735 ..

Align seg 1/1 to: AAY50735 from: 1 to: 441

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38  ATGGTGGCCACCAAAATGCTGCTTTCTGCTGCTGGCTGGCTGGC 87
1  MetValProLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17
88  TGTGGTTTATCCTTTTGTGCTGCAATACATAAATCCTGTTGGCCATATGA 137
17  aValValTyrProPheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
138  AATATPACGATGGGTCAACAAATACAGTACTGATGCTGCTGCAAGC 187
34  ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50
188  TTTGGCCAACTAAATCCCGGGGAATGGGCTTATTCCGCTGGTGG 237
51  PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
238  TACAGACTTAATGTTTGATCACACTAATAAGGCGACCTTTCTGCGTTAT 287
67  sthrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84
288  ATTATCCATCCCAAGATATGATCGCTTGACACCTTTGGATCCCAAT 337
84  yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100
338  AAAGATATTTTGGGCTCTTACCAATTTCTTGGACACACTGGCTTAT 387
101  LysGlyTyrPheTrpGlyLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
388  GGGCAACATTTTGGGTTACTCTTGGTTCAATGACAACTCCTGCAAACT 437

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117  tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsnT 134
438  GGAATTCCTCCCTCTGAGCGCTGGTGAATAATATCCACTTGTGTTTCT 487
134  rPasnSerProLeuArgProGlyGlyLysTyrProLeuValValPheSer 150
488  CATGGTCTTGGGCACTTACAGACACTTTATTCGCTATTGGCAATGACCT 537
151  HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
538  GGCATCTCATGGGTTTATAGTCTGCTGTAGACACAGACAGATAGATCTG 587
167  uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSerA 184
588  CATCTCTCAACTTACTATTCAAGGACCAATCTGCTGCAGAAATAGGGGAC 637
184  laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200
638  AAGTCTTGGCTCTACCTTAGAACCTGAAACAGAGAGGAGGAGACATAT 687
201  LysSerTrpLeuTyrLeuArgThrLeuLysGlnGluGluThrHisIle 217
688  ACGAATGACGAGTACGCGCAAGAGCAAAAGATCTTCCCAAGCTCTCA 737
217  eArgAsnGluGlnValArgGlnArgAlaLysGluCysSerGlnAlaLeuS 234
738  GTCGTGATCTTGACATTCATGGAAGCCAGTGAAGATGCAATGCAATGAT 787
234  erLeuIleLeuAspIleAspHisGlyLysProValLysAsnAlaLeuAsp 250
788  TTAAGTTTGGATATGGAACAACTGAAGGACTCTATTGATGGGAAAAAAT 837
251  LeuLysPheAspMetGluGlnLeuLysAspSerIleAspArgGluLysIle 267
838  AGCAGTAATTTGGCACTTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTA 887
267  eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 284
888  GTGAAGATCAGAGATTCAGATTCGCTGTTGCTGGATGCTGATGTTT 937
284  erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
938  CCAGTGGTGTGATGAAGTATATTCAGAAATTCCTCAGCCCCCTCTTTTAT 987
301  ProLeuGlyAspGluValTyrSerArgIleProGlnProLeuPhePheIle 317
988  CAACTCTGAATATTTCCAATATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1037
317  eAsnSerGluTyrPheGlnTyrProAlaAsnIleIleLysMetLysLysC 334
1038  GCTACTCACCTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 1087
334  ystYrSerProAspLysGluArgLysMetIleThrIleArgGlySerVal 350
1088  CACCAAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
351  HisGlnAsnPheAlaAspPheThrPheAlaThrGlyLysIleIleGlyHi 367
1138  CATGCTCAAAATTAAGGGAGACATAGATTCAATCCAGCTATTGATCTTA 1187
367  smetLeuLysLeuLysGlyAspIleAspSerAsnValAlaIleAspLeuS 384
1188  GCAACAAGCTTCATTAGCATTTCTTACAAAAGCAATTTAGGACTTTCATAAA 1237
384  erAsnLysAlaSerLeuAlaPheLeuGlnLysHisLeuGlyLeuHisLys 400
1238  GATTTTTCATCAGTGGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
401  AspPheAspGlnTrpAspCysLeuIleGluGlyAspAspGluAsnLeuIle 417
1288  TCCAGGGGACCAACATTAACACCAACCAACATCAACACATCATGTTACAGACT 1337

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417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434

1338 CTTGAGGAATAGAGAAATACAAT 1360

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434 eSerGlyIleGluLysTyrAsn 441

seq_name: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:AAE00761

seq_documentation_block:

ID AAE00761 standard; Protein: 441 AA.

AC AAE00761;

XX 02-JUL-2001 (first entry)

DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
KW antinflammatory; septicemia; inflammation; haemostasis; parturition;
KW asthma; anaphylaxis; septic shock; antibacterial.

OS Homo sapiens.

XX Key Location/Qualifiers

PH Peptide 1..41 "Hydrophobic segment containing 1-17 amino acids
FT of signal sequence plus an additional peptide that is
FT cleaved to yield the mature functional enzyme"

FT Protein 42..441

FT /label= Mature_human_PAF-AH_peptide

FT Domain 271..275

FT /label= Consensus_motif

PN USG203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

PR 22-JAN-1998; 98US-0010715.

PR 06-OCT-1993; 93US-0133803.

PR 06-OCT-1994; 94US-0318905.

PA (ICOS-) ICOS CORP.

XX Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

PI Wilder CL;

XX WPT; 2001-280610/29.

DR N-PSDB; AAD04143.

XX Treating a mammal susceptible to or suffering from septicemia comprises
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT supplement endogenous PAF-AH activity and to inactivate pathological
PT amounts of PAF

PS Claim 1; Column 47-50; 54pp; English.

XX The present sequence is human plasma platelet-activating factor

CC acetylhydrolase (PAF-AH) protein.

CC The invention relates to human plasma platelet-activating factor

CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to

CC or suffering from septicemia. PAF functions in normal physiological

CC processes such as inflammation, haemostasis and parturition. PAF-AH

CC specific antibodies are used in the diagnostic methods to detect abnormal

CC levels of PAF-AH in serum and also for treating the pathological

CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic

CC shock and arthritis. PAF-AH antibody is also useful for screening a

CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the

CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human
CC plasma PAF-AH gene.

XX Sequence 441 AA;

SQ

alignment_scores:

Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x AAE00761

Align seq 1/1 to: AAE00761 from: 1 to: 441

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88 TGTGGTTTATCTTTGACTGCGCAATACATAAATCCTGTGGCCATATGA 137
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17 aValValTyrProPheAspTyrGlnTyrIleAsnProValAlaHisMetL 34
138 AATCATCAGCATGGTCAACAAATACAACTGATGCTGCTGCTGCAAGC 187
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34 ysSerSerAlaTyrValAsnLysIleGlnValLeuMetAlaAlaSer 50
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|||||
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
238 TACAGACTTAATGTTTGCATCACACTAATAAGGGCACCTTCTTGCCTTAT 287
|||||
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84
288 ATTATCCATCCCAAGATAATGATCGCCTTGACACCTTTGGATCCCAAT 337
|||||
84 yTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100
338 AAGATATATTTTGGGTCTTAGCAAAATTTCTTGGACACACTGCTTAT 387
|||||
101 LysGluTyrPheTyrPheLeuSerLysPheLeuGlyThrHisTrpLeuMe 117
388 GGGCAACATTTTGAGGTACTTTTGTGTTCAATGACAACTCTGCAAACT 437
|||||
117 tGlyAsnIleLeuArgLeuPheGlySerMetThrThrProAlaAsnT 134
438 GGAATTCCTCTCTGAGGCCTGGTGAATAATATCCACTTGTGTTTTTCT 487
|||||
134 rpAsnSerProLeuArgProGlyGlyLysTyrProLeuValValPheSer 150
488 CATGCTCTGGGGCATTCAGGACACTTATTTCTGCTATTGGCATTGACCT 537
|||||
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
538 GGCATCTCATGGTWTATAGTGTGCTGTAGACACAGACAGATAGATCTG 587
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167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSerA 184
588 CATCTGCAACTTACTATTTTCAAGGACCAATCTGCTGAGAAATAGGGGAC 637
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184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200
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688 AGCAATAGGAGGTAGCGCAAGAGACAAAGAAATGTTCCCAAGCTCTCA 737
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738 GTCTGATTCTTGACATTGATCATGTGAAGCCAGTGAAGATGCATTAGAT 787

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788 TTTAAAGTTTGTATGGACAACTGAAGACTCTCTATTGATAGGAAAAAT 837
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838 AGCAGTAATTTGGACATCTTTTGTGTGGAGCAACGGTTATTGAGACTCTTA 887
267 eAlaValIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeu 284
888 GTGAAGATCAGAGATTTCAGATCTGCTGTTTCCCTGGATGCTGGATGTT 937
284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
938 CCACTGGGTGATGAAGTATATCCAGAAATTCCTCAGCCCTCTTTTATTAT 987
301 ProLeuGlyAspGluValTySerArgIleProGlnProLeuPhePheI 317
988 CAACCTGAATATTTCCTAATATCTGCTTAATATCATATAAAATGAAAAAT 1037
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ID AAB49451 standard; Protein; 441 AA.
XX AC AAB49451;
XX DT
XX DE
XX DE Platelet-activating factor acetylhydrolase.
XX KW PAF-AH; antiallergic; antiinflammatory; platelet-activating factor;
XX KW PAF-acetylhydrolase; enzyme; pleurisy; asthma; rhinitis; human;
XX KW necrotizing enterocolitis; acute respiratory distress syndrome.
XX OS Homo sapiens.
XX PN US6146625-A.
XX PD 14-NOV-2000.
XX PF 22-JAN-1998; 98US-0010715.

XX 07-JUN-1995; 95US-0480658.
PR 06-OCT-1993; 93US-0133803.
PR 06-OCT-1994; 94US-0318905.
XX (ICOS-) ICOS CORP.
XX Gray P, Trong HL, Tjoelker LW, Wilder CL, Eberhardt CD;
PI Cousins LS;
XX WPT; 2001-040421/05.
DR N-PSDB; AAC89057.
XX Treating platelet-activating factor mediated pathologies such as
PT asthma, rhinitis, pleurisy and acute respiratory distress syndrome
PT comprising administering platelet-activating factor acetylhydrolase
PT enzyme
XX Claim 1; Column 47-50; 54pp; English.
XX The present invention relates to a method for treating a mammal
CC susceptible to or suffering from a platelet-activating factor
CC (PAF)-mediated pathological condition, comprising administering a
CC composition comprising PAF acetylhydrolase (PAF-AH) enzyme to
CC supplement endogenous PAF-AH activity and to inactivate pathological
CC amounts of PAF in the mammal. PAF-mediated pathological conditions
CC are conditions such as pleurisy, asthma, rhinitis, necrotizing
CC enterocolitis and acute respiratory distress syndrome in mammals.
CC The present sequence is human PAF-AH.
XX SQ Sequence 441 AA;
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seq_documentation_block:

ID AAR71920 standard; Protein; 441 AA.

XX AAR71920;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant SI08A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 108

XX /note= "Wild-type Ser is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
acetylhydrolase - useful in diagnosis and for treating
inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
made with single amino acid changes for the purposes of identifying
the active site of AH. The sequences of these mutants are not given
in the patent specification; they have been derived from the original
wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory
diseases, in particular pleurisy, asthma, rhinitis and eczema. The
gene may also be used in raising monoclonal antibodies specific for AH
that are useful in the diagnosis of such diseases.

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; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
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; APPLICATION NUMBER: US 08/133,803
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; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
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Patent No. 5656431
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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US-08-483-232-8

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; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolyase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-8

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; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-041-8

alignment_scores:
Quality: 2354.00 Length: 441
Ratio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.773

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seq_documentation_block:
; Sequence 8, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-328-474-8

alignment_scores:
Quality: 2354.00 Length: 441
Ratio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.773
alignment_block:
US-09-922-067-9 x US-09-328-474-8
Align seg 1/1 to: US-09-328-474-8 from: 1 to: 441

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seq_documentation_block:
; Sequence 8, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,803
 FILING DATE: 06-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 6099836and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32793
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 441 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-100-546-8

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 Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773
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 : Sequence 8, Application US/09010715
 : Patent No. 6146625
 : GENERAL INFORMATION:
 : APPLICANT: Cousens, Lawrence S.
 : APPLICANT: Eberhardt, Christine D.
 : APPLICANT: Gray, Patrick W.

APPLICANT: Le Trong, Hai
 APPLICANT: Tjoelker, Larry W.
 APPLICANT: Wilder, Cheryl L.
 TITLE OF INVENTION: Platelet-Activating Factor
 TITLE OF INVENTION: Acetylhydrolase
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/010,715
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 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/133,803
 FILING DATE: 06-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6146625and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32793
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 441 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PS-09-010-715-8

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Quality:	2354.00	Length: 441
Ratio:	5.338	Gaps: 0
Percent Similarity:	100.000	Percent Identity: 99.773

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; Sequence 8, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
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; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE:
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; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-577-758-8

alignment_scores:

Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.773
alignment_block:
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1 MetValProPheLysLeuHisValLeuPheCysLeuCysGlyCysLeuAl 17
88 TGTGGTTTATCCTTTGACTGGCAATACATAAATCCCTGTTGCCCATATGA 137
17 aValValTyrPropheAspTrpGlnTyrIleAsnProValAlaHisMetL 34
138 AATCATCAGCATGGGTCAACAAATAACAAGTACTGATGGCTGCTCCAAGC 187
34 ysSerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaAser 50
188 TTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCCGTTGGTTG 237
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
238 TACAGACTTAATGTTGATCACACTAATAAGGGCACCTTCTTGGCTTTAT 287
67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeuT 84
288 ATTATCCATCCCAAGATATATGATCGCTTGACACCCCTTTGGATCCCAAT 337
84 yrTyrProSerGlnAspAsnAspArgLeuAspThrLeuTrpIleProAsn 100
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388 GGGCAACATTTTTCAGCTTACTCTTTGGTTCATGACAACTCCTGCAAACT 437
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438 GGAATTCCTCTGAGGCTGGTGAANAATATCCACTTGTGTTTTTCT 487
134 rPAsnSerProLeuArgProGlyGlyLysTyrProLeuValValPheSer 150
488 CATGCTCTTGGGCAATTCAGGACACTTTATTCTGCTATTGGCATTGACT 537
151 HisGlyLeuGlyAlaPheArgThrLeuTyrSerAlaIleGlyIleAspLe 167
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167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspArgSera 184
588 CATCTGCAACTTACTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGAC 637
184 laSerAlaThrTyrTyrPheLysAspGlnSerAlaAlaGluIleGlyAsp 200
638 AAGTCTTGGCTCTACCTTAGAACCCCTGAACAAGAGAGGAGGAGACACAT 687
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251 LeuLysPheAspMetGlnGlnLeuLysAspSerIleAspArgGluLysI 267
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267 ealavalleGlyHLSerPheGlyAlaThrValIleGlnThrLeuS 284
888 GTGAAGATCAGAGATTCAGATGTGTATTTGGCCCTGGATGCATGGATGTTT 937
284 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspAlaTrpMetPhe 300
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seq_documentation_block:
; Sequence 33, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-938A-33

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Quality: 1964.50 Length: 442
Ratio: 4.677 Gaps: 1
Percent Similarity: 95.023 Percent Identity: 82.353

alignment_block:
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17 aLeuValTyProPheAspTrpGlnAspLeuAsnProValAlaTyIleG 34
138 AATCATCAGCATGGGTCAACAAATACAACTACTGCTGCTGCTCAAGC 187
34 LuSerProAlaTrpValSerLysIleGlnAlaLeuMetAlaAlaAlaAsn 50
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67 sThrAspLeuMetPheAspTyThrAsnLysGlyThrPheLeuArgLeuT 84
288 ATTATCCATCCACAGATTAATGATCCCTTGCACACCTTTGGATCCCAAT 337
84 yTyTyProSerGlnAspAspHisSerAspThrLeuTrpIleProAsn 100
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388 GGGCAACATTTTGGGTGTACTCTTTGGTTTCAATGACAACTCTCGAAACT 437
117 lGlyLysIleMetGlyLeuPhePheGlySerMetThrThrProAlaAlaT 134
438 GGAATTCCTCTGAGCGCTGGTGAATAATATCCACTTCTGTTGTTTCT 487
134 rAsnAlaHisLeuArgThrGlyGluLysTyProLeuIleIlePheSer 150
488 CATGCTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTCACCT 537
151 HisGlyLeuGlyAlaPheArgThrIleTySerAlaIleGlyIleAspLe 167

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seq_documentation_block:
; Sequence 28, Application US/08483140
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alignment_scores:
  Quality: 1935.50      Length: 442
  Ratio: 4.686          Gaps: 1
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alignment_block:
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Align seg 1/1 to: US-08-483-140-28 from: 1 to: 444

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88 TGTGGTTTATCCTTTGACTGGCAATACATAAAATCCTCTTGCCCATATCA 137
17 rLeuValHisProIleAspTrpGlnAspLeuAsnProValAlaHisIleA 34
138 AATCATCAGCAGTGGTCAACAAATACAACTACTGATGCTGCCTCGCAAGC 187
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438 GAATTCCTCCCTGAGGCTGGTGAATAATCCACTTGTCTTTTCT 487
134 rpaSerProLeuArgThrGlyGluLysTyrProLeuIleValPheSer 150
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151 HisGlyLeuGlyAlaPheArgThrIleTyrSerAlaIleGlyIleAspLe 167
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588 CATCTGCAACTTACTATTTCAGGACCAATCTGTCGACAAATAGGGGAC 637
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234 euAsnLeuIleLeuAspIleAspHisGlyArgProIleLysAsnValLeu 250
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835 AATACAGTAATGGACATCTTTTGGTGAGCAACGGTTATTACAGACTC 884
267 sIleAlaValIleGlyHisSerPheGlyGlyAlaThrValLeuGlnAlaL 284
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seq_documentation_block:
; Sequence 32, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-32
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alignment_scores: Quality: 1935.50 Length: 442

Ratio: 4.686 Gaps: 1
Percent similarity: 93.439 Percent identity: 80.769
alignment_block:
US-09-922-067-9 x US-08-485-938A-32 ..
Align seg 1/1 to: US-08-485-938A-32 from: 1 to: 444

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1 MetLeuProProLysLeuHisAlaLeuPheCysLeuCysSerLeuTh 17
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; Sequence 27, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/133,803

FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5698403and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32781

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 440 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-140-27

alignment_scores:

Quality: 1515.50 Length: 442

Ratio: 4.031 Gaps: 2

Percent Similarity: 85.068 Percent Identity: 66.516

alignment_block:

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Align seg 1/1 to: US-08-483-140-27 from: 1 to: 440

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seq_documentation_block:

; Sequence 31, Application US/08485938A

; Patent No. 5847088

; GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.

; APPLICANT: Eberhardt, Christine D.

; APPLICANT: Gray, Patrick W.

APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-31

alignment_scores:
Quality: 1515.50 Length: 442
Ratio: 4.031 Gaps: 2
Percent Similarity: 85.068 Percent Identity: 66.516

alignment_block:

US-09-922-067-9 x US-08-485-938A-31 ..

Align seg 1/1 to: US-08-485-938A-31 from: 1 to: 440

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88 TGTGGTTTATCCTTTTGAAGTGGCAATACATAAATCCTGTTGCCCATATGA 137
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17 orPValHisProPheHisTrpGlnAspThrSerSerPhe....AspPheA 33
138 AATCATGACATGGGTGCAACAAATACAACTAGTGTGCTGCTGCTGCAAGC 187
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688 ACCAATGACGAGTACGGCNAAGAGCAAAAGATGTTCCCAAGCTCTCA 737
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OM of: US-09-922-067-9 to: PIR_68:* out_format : pfs

Date: Mar 9, 2002 12:25 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=framet_n2p_model -DEV=xlp
-Q/cgnt2_1/USPTO-spoon/US09922067/runat_07032002_140445_931/app_query.fasta_1.1439
-DB=PIR_68 -QMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-QAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Search information block:

Query: US-09-922-067-9
Query length: 1361
Database: PIR_68:*
Database sequences: 219241
Database length: 76174552
Search time (sec): 96.640000

score_list:

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pir2:T28936	+ 493.50	736.48	1.0e-33	476	hypothetical protein C52B9.7
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pir2:F82858	+ 148.50	208.03	0.0002	795	dipeptidyl-peptidase XE0015 [f]
pir2:JN0490	+ 120.50	173.59	0.0360	310	28K lipase precursor - Streptomyces
pir2:S75452	+ 119.00	165.33	0.0518	622	hypothetical protein sir1506 -
pir2:D75217	+ 112.00	161.37	0.1871	286	probable 2-acetyl-1-alkylglycerol
pir2:S66261	+ 110.50	151.27	0.2751	711	X-Pro dipeptidyl-peptidase (EC
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pir2:A86511	+ 106.50	153.36	0.5442	275	acyltransferase family [importe
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pir2:G82193	+ 104.50	140.44	0.9036	868	aminopeptidase N VC1494 [import
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pir2:T15247	+ 100.00	138.80	2.04	474	hypothetical protein T05E7.1 -
pir2:T41703	+ 100.00	134.38	2.15	793	dipeptidyl aminopeptidase - fli
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pir2:C82418	+ 98.00	133.36	3.10	627	GGDEF family protein VCA0785 [f
pir2:S76481	+ 97.50	133.92	3.37	538	hypothetical protein - Synchoc
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pir2:A71556	+ 95.00	129.64	5.51	569	probable S1 ribosomal protein -
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pir2:E96803 + 93.00 130.02 7.81 382 ! probable lipase, 4162-5963
pir2:T34457 + 93.00 127.16 8.08 533 ! hypothetical protein T19H12
pir2:G41426 + 93.00 126.99 8.09 544 ! carboxylesterase (EC 3.1.1.1)
pir2:G84601 + 93.00 122.94 8.49 871 ! probable protein kinase [im

seq_name: pir2:S60247

seq_documentation_block:

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

R:Jfoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf,

W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

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Quality: 2354.00 Length: 441

Ratio: 5.338 Gaps: 0

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alignment_block:

US-09-922-067-9 x S60247 ..

Align seg 1/1 to: S60247 from: 1 to: 441

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88 TGTGCTTTATCCTTTGACTGGCAATACATAAATCTGTTGCCCATATGA 137
|||||
17 aValVallyrProPheAspTrpGlnTrpIleAsnProValAlaHisMetL 34
138 AATCATGACATGGGTCAACAAATACAGTACTGATGGTGGTGGCAAGC 187
|||||
34 ySerSerAlaTrpValAsnLysIleGlnValLeuMetAlaAlaSer 50
188 TTTTGGCCAACTAAATCCCGGGGAAATGGGCCTTATTCCGTTGGTTG 237
|||||
51 PheGlyGlnThrLysIleProArgGlyAsnGlyProTyrSerValGlyCy 67
238 TACAGACTTAATGTTTGATCACACTAATAAGGGCACCTTTCTCGGTTAT 287
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67 sThrAspLeuMetPheAspHisThrAsnLysGlyThrPheLeuArgLeu 84
288 ATTATCCATCCCAAGATAATGATGCGCTTCACACCCCTTGGATCCCAAT 337
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117 tGlyAsnIleLeuArgLeuLeuPheGlySerMetThrThrProAlaAsn 134
438 GGAATTCCTCTGAGGCTGTTGAGAAAATATCCACTTGTGTTTTCCT 487
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134 rpAsnSerProLeuArgProGlyGlyLysTrpProLeuValValPheSer 150
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888 GTGAAGATCAGAGATTCAGATGTTGTTGCTGGAGCAAGCGTTATTTCAGACTCTTA 937
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417 eProGlyThrAsnIleAsnThrThrAsnGlnHisIleMetLeuGlnAsnS 434
|||||
1338 CTTTCAGGAATAGAAATACAAT 1360
|||||
434 erSerGlyIleGluLysTyrrAsn 441
|||||

seq_name: pir2:JC5021

seq_documentation_block:

platelet-activating factor-acetylhydrolase (EC 3.1.1.1) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase
C:Species: Cavia porcellus (guinea pig)
C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000
C:Accession: JC5021; PC4207
R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yoo
J. Biochem. 120, 838-844, 1996
A:Title: Cloning, expression and characterization of plasma platelet-activating f
A:Reference number: JC5021; MUID:97103479
A:Accession: JC5021
A:Molecule type: DNA
A:Residues: 1-436 <KARI>
A:Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:g1644229
A:Accession: PC4207
A:Molecule type: protein
A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-3
A:Experimental source: liver
C:Comment: This enzyme converts platelet-activating factor to an inactive metabol
C:Keywords: glycoprotein; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <M
F:76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

alignment_scores:

Quality: 1572.50 Length: 441
Ratio: 4.022 Gaps: 2
Percent Similarity: 88.662 Percent Identity: 66.213

alignment_block:

US-09-922-067-9 x JC5021

Align seg 1/1 to: JC5021 from: 1 to: 436

38 ATGGTGGCCACCCAAATTCATGTCGCTTTCTGCTCTGCGGCTGCCGTGGC 87
|||||
1 MetAlaProProLysLeuHisThrLeuPheCysLeuSerGlyPheLeuAl 17
88 TGTGCTTTATCCTTTTGGCTGGCAATACATAAATCCTGTGTGCCCATATGA 137
|||||
17 aLeuValHisProPheAspTrpArgAspLeuAspProValThrTyrrIleG 34
|||||
138 AATCATCAGCATGGGTCAACAAATACAACTACTGATGGCTGCTGCAAGC 187
|||||
34 InSerSerValTrpIleGlnArgIleGlnSerGluLeuLeuIleThrSer 50
188 TTTGGCCAACTAAATCCCGGGGAATGGCCCTTATTCGCTGGTTG 237
|||||
51 PheGlyHisThrThrIleProLysGlyAsnGlyProTyrrSerValGlyCy 67
238 TACAGACTTAATGTTTGTATCACACTAATAAGGCACCTCTTTCGCTTTAT 287
|||||
67 sThrAspLeuMetSerGlyTyrrThrAsnGlnSerSerPheLeuArgLeu 84
288 ATTATCATCCACAGATATGATCGCTTGGACACCTTTGGATCCCAAT 337
|||||
84 yrTyrrProSerGlnAspAsnAspPheProAspAlaLeuTrpIleProAsn 100
338 AAAGAATATTTTGGGCTCTTAGCAAAATTTCTTGGACACACTGGCTTAT 387
|||||
101 GluGluTyrrPheGlnGlyLeuThrGluThrLeuGlyAlaSerSerPheLe 117
388 GGCAACATTTTGGGTTACTCTTTGGTTCAATGACAACTCTCTGCAAACT 437
|||||
117 uGlyLysLeuLeuLysLeuLeuTyrrGlySerValLysValProAlaLys 134
438 GGAATTCCTCTCTGAGGCTGGTGAATAATATCCACTTGTGTTTTCT 487
|||||
134 rpAsnSerProLeuLysThrGlyGluLysTyrrProLeuIlePheSer 150
488 CATGGCTTGGGCTTCAGGACACTTATTCTGCTATTGGCATTCACCT 537
|||||
151 HisGlyLeuGlyAlaPheArgSerIleTyrrSerAlaIleGlyIleGluLe 167

538 GGCATCTCATGGGTTTATAGTTGCTGTAGAACACAGACATAGATCTG 587
 167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspGluSerA 184
 588 CATCTGCAACTTACTATTTCAGGACCAATCTGTCGAGAAATAGGGAC 637
 184 laAlaAlaThrTyrPheGlnAspAlaProAlaAlaGluSerGlyAsn 200
 638 AAGTCTTGGCTCTACCTTAGAACCTGAAACAGAGGAGGAGACACATAT 687
 201 ArgSerPheIleTyrLysVal.....GlyAsnLeuGluThrGluG 215
 688 ACAGAAATGACAGGTAGCGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCA 737
 215 uArgLysArgGlnLeuArgGlnArgGlyGluGluCysSerGlnAlaLeuS 232
 738 GTCTGATCTTGACATTGATCATCGAAGCCAGTGAAGATGCATTAGAT 787
 232 erTrpLeuLeuSerIleAspGluGlyGluProValLysAsnValLeuAsp 248
 788 TTAAGTTTGCATATGGAACCACTGAAGGACTCTATTGATAGGAAAAAAT 837
 249 LeuAsnPheAspIleGlnGlnLeuLysGlySerLeuAspArgSerLysVa 265
 838 AGCAGTAATTTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTA 887
 265 laIleIleGlyHisSerPheGlyGlyAlaThrValIleGlnThrLeuS 282
 888 GTGAAGATCAGAGATTCAGATGCTGGTATTGCCCTGGATGCATGATGTTT 937
 282 erGluAspGlnArgPheArgCysGlyIleAlaLeuAspProTrpMetPhe 298
 938 CCAGTGGTGTAGTAAATATTCAGAAATTCCTCAGCCCTCTTTTAT 987
 299 ProValGlyGluAspValHisSerLysIleProGlnProLeuPhePheI 315
 988 CAAGTCTGAATATTTCCAAATATCTCGTGAATATCATATAAAATGAAAAAT 1037
 315 eAsnSerGluTyrPheGlnSerAlaAsnAspThrLysLysIleGluLysP 332
 1038 GCTACTCACCTGATAAAGAAAGATGATGATACAAATCAGGGTTCAGTC 1087
 332 heTyrGlnProGlnLysGluArgLysMetIleAlaValLysGlySerVal 348
 1088 CACAGAAATTTGCTGACTTCACATTTGCAACTGGCAAAATAATGGACA 1137
 349 HisHisAsnPheValAspPheThrPheAlaThrGlyLysIleIleGly 365
 1138 CATGCTCAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTA 1187
 365 nMetLeuSerLeuLysGlyLysIleAspSerGluValAlaMetAspLeuI 382
 1188 GCACAAAGCTTCATTACATCTTACAAAGCATTTAGGACTTCATATAA 1237
 382 LeAsnLysAlaSerLeuAlaPheLeuGlnLysTyrLeuGlyLeuAspLys 398
 1238 GATTTTGATCAGTGGAGCTGCTTGATTGAAGGAGATGATGAGAATCTTAT 1287
 399 AsnPheAspGlnTrpAsnSerLeuMetGluGlyAspGluAsnLeuI 415
 1288 TCCAGGGACCAACATTAACAACAACCAATCAACACATCATGTTTACAGAAT 1337
 415 eProGluPheThrIleProThr.....MetGlnSerS 427
 1338 CTTTCAGGAATACAGAAATACAAAT 1360
 427 erThrGlyThrGluGlnArgAsn 434

seq_name: pir2:T32756

seq_documentation_block:

hypothetical protein W03G9.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32756
 R:Dante, M.; Keppler, D.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid W03G9.
 A:Reference number: 221220
 A:Accession: T32756
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-384 <DAN>
 A:Cross-references: EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN00019; CESP:W03G9.6
 A:Experimental source: strain Bristol N2; clone W03G9
 C:Genetics:
 A:Gene: CESP:W03G9.6
 A:Map position: 1
 A:Introns: 47/3; 90/2; 142/2; 183/3; 333/3

alignment_scores:
 Quality: 497.00 Length: 348
 Ratio: 2.097 Gaps: 9
 Percent Similarity: 68.103 Percent Identity: 33.908

alignment_block:
 US-09-922-067-9 x T32756 ..

Align seg 1/1 to: T32756 from: 1 to: 384

200 AAATCCCGGGGAAATGGCCTTATTCCGTTGGTTGTACAGACTAAT 249
 14 LysMetPro.....GlyGlnPheLysValGlyCysMetAspLeuMe 27
 250 GTTTGATCAC...ACTAATAAGGGCACCTTCTTGGTTCGTTTATATATCAT 296
 27 tiledGluGluAlaAlaGlySerGlyLeuPheMetArgLeuPhePheProt 44
 297 CCCAAGATAATGATCCCTTGAC.....ACCCCTTGGATCCCCA 334
 44 ...AspSerGluIleThrGlyProSerSerLeuProValTrpIlePro 59
 335 ATAAGAATAATTTTGGGCTCTTAGCAAAATTTCTTGA...ACACACTG 381
 60 ArgProGluTyrAlaTyrGlyValGlyGlyLeuGlyHisSerProH 76
 382 GCTTATGGCAACATTTGAGTTTACTCTTGGTTCAATGACAACTCCTG 431
 76 sGlnMetAspLeuIleSerSerLeuValIleGlyAspLysArgValAspC 93
 432 CAAACTGGAAATCCCTCTCTG...AGGCCTGGTGAATAATATCCACTGTT 478
 93 ystleAspAsnAlaGlnLeuSerThrLysSerAspLysTrpProValLeu 109
 479 GTTTTTTTCATGCTCTGGGCAATTCAGCACACTTTTATTCTGCTATTGG 528
 110 ValPheSerHisGlyLeuGlyGlySerArgThrPheTyrSerThrTyrCy 126
 529 CATGTACCTGGCATCTCATGGTTTATAGTTGCTGTAGAACACAGAG 578
 126 sThrSerLeuAlaSerHisGlyTyrValValAlaAlaValGluHisArg 143
 579 ATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGTCGACAA 628
 143 spSerAlaCysTrpThrTyrLysLeuValGluLysAsnGlyThrLeu 159
 629 ATAGGGGACAAAGTCTTGGCTCTACCTTAGAACCTGAAACAAGAGGAGGA 678
 160 ValGluLysProMetLysIleLysLeuValAspArgAsnAspLysAspGI 176
 679 GACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCC 728
 176 nPheLysIleArgAsnGluGlnValGlyLysArgAlaGluGluCysAlaL 193
 729 AAGCTCTCAGTCTGATTCTTTGACATTCATGATGAAAGCCAGCATGAAGAAT 778

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195 ysAlavallyslleleuGluInleuAspSerGlyAsn...ValLysAsp 208
779 GCATTAGATTTA.....AAGTTTGATATGCAACAACCTGAAGGACTCTAT 822
209 LysValilleleGlyAsnAsnAlaAsnLeuGluPhePheLysAsnLysLe 225
823 TCATAGGGGAAAAAATAGCAGTAATTCGACATCTTTTGGTGGAGCAACGG 872
225 uleuthrThrAlaSerlleleGlyHisSerPheGlyAlaIaThrs 242
873 TTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGATGTGTGATTCGCTG 922
242 erilleAlaSerSerSerAsp.....PheGlnLysAlaIleValLeu 256
923 GATGCATGATGTTTCCACTGGGTGATGAATATATCCAGAAATTCCTCA 972
257 AspGlyTyrMetTyrProLeuAspGlnAsnGlnGlnGluInAlaLysG 273
973 GCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCA 1022
273 nProileMetPheLeuAsnValGlyAspTrpGlnTrpAsnGluAsnLeu 290
1023 TAAAAATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACA 1072
290 luValMetargLyslleleuProAsnAsnGluGlyAsnleleuLeuThr 306
1073 ATCAGGGTTCAGTCCACCAGAAATTTGCTGATCTTCACATTTTGCACCTG 1122
307 LeuSerGlyAlaValHisGlnSerPheThrAspPheProPheValPhePr 323
1123 CAAATAATTTGGACACATGCTCAATTTAAAGGGAGACATAGATTCAAATG 1172
323 oAsnTrpLeuAlaLysGlnPheGlyValHisGlyProThrGluProTyrL 340
1173 CAGCTATTGATCTTAGCAACAAGCTTCATTAGCATTTCTTACAA 1216
340 euCysMetGlnSerAlaIleGluLeuThrLeuSerPheLeuLys 354
seq_name: pir2:T28936
seq_documentation_block:
hypothetical protein C52B9.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28936
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: 220545
A:Accession: T28936
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-476 <NEL>
A:Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN00028; CESP:C52B9.7
A:Experimental source: strain Bristol N2, clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.7
A:Map position: X
A:Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

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alignment_scores:

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Quality: 493.50      Length: 383
Ratio: 2.127         Gaps: 8
Percent Similarity: 60.574      Percent Identity: 32.115

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alignment_block:

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US-09-922-067-9 x T28936

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Align seg 1/1 to: T28936 from: 1 to: 476

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146 GCATGGGTCAACAAAATACAAAGTACTGATGCTGCAAGCTTTGGCCA 195

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75 SerTyrIleSerSerProGlnValLeuThrArgGlnValSer..... 88
196 AACTAAATCCCGGGGAAATGGCCCTTATTCGGTGGTGTACAGACT 245
89 .....GlyGlnPheGlnValGlyCysLysAspL 98
246 TAATGTTTGATCACACT.....AATAAGGGCACCTTCTTGGCTTTA 286
98 euMetIleAspGlyThrValLeuGlyAspArgGlyLeuPheMetArgLeu 114
287 TATTATCCATCCCAAGATAATGATCGCCTTCAC.....ACCTT 324
115 TyrPheProThr...AspSerGlnAlaAlaAspIleSerSerTyrProLe 130
325 TTGGATCCCAATAAAGAAATATTTTGGGCTCTTAGCAAAATTCCTGA 373
130 utrPLeuProLysProGlnTyrAlaHisGlyLeuGlyGluTyrLeuGly 147
374 ..ACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTTCATG 421
147 InSerSerGlnLysMetAsnValIleThrSerThrValValGlyGluLys 163
422 ACAACTCTCTGCAACTGGAATTCCTCTCGAGGCTGGT...GAAAAATA 468
164 ArgGluAspCysIleGluAsnAlaGlnMetSerThrLysCysAspLysTr 180
469 TCCACTTGTGTTTTCATCGTCTTGGGCACTTCAGGACACTTATT 518
180 pProIleValValPheSerHisGlyLeuGlyGlySerArgThrPheTyrS 197
519 CTGCTATTGGCATTCACCTGGCATCTCATGGGTTTATAGTTGCTGCTGA 568
197 erThrTyrCysThrSerLeuAlaSerHisGlyTyrValValAlaIaVal 213
569 GAACAC..... 574
214 GluHisLysTrpGlyLysSerGlyGlyArgCysAspHisValAlaPheSe 230
575 ....AGAGATAGATCTGCATCTGCAACTTACTATTTCACAGGACCACTG 620
230 rCysArgAspHisSerAlaCysTrpThrTyrGlnLeuThrGluLysAsnG 247
621 CTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAACCCCTGAAACAA 670
247 LyGluLeuValGluGlnProIleLysIleLysLeuIleGluLysAsnGlu 263
671 GAGGAGGACACATATACGAAATAGCAGGTACGGCAAGAGACAAAGA 720
264 LysAsnGluPheLysIleArgAsnGlnValGlyLysArgValThrGl 280
721 ATGTTCCCAAGCTCTCAGTCTCATTTCTTGCATTCATGATGATGGAAG...C 767
280 ucysValLysAlaLeuAsnValLeuGluGlnLeuAsnLeuGlyThrValP 297
768 CAGTGAAGATGCATTAGATTATAAGTTTGAATGGAACAACCTGAAGGAC 817
297 roGluLysValLeuIleGlyAsnAspTyrAsnTrpAlaGlnPheLysAsn 313
818 TCTATTGATAGGGAAAAAATAGCAGTAATTCGACATTCCTTTGGTGGAGC 867
314 LysLeuValMetSerSerAlaSerValIleGlyHisSerPheGlyGlyAl 330
868 AACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGTTGTTG 917
330 aThrSerLeuAlaSerSerAlaTyrThrThrAspPheGlnLysAlaIleV 347
918 CCCTGGATGATGATGTTTCCACTGGGTGATGAAGAGTATATATCCAGAAAT 967
347 alpheAspGlyTyrMetTyrProLeuAspSerThrGlnGlnGluGlnAla 363
968 CCTCAGGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCCTCTAA 1017

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seq_name: pir2:T39268

seq_documentation_block.
hypothetical protein SPBC106.11c - fission yeast (Schizosaccharomyces pombe)

C:species: scirizosaccaromyces pombe
C:Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 03-Dec-1999

C;ACCESSION: T39268
R:Lyne, M.: Rajadream M.A.: Barrell, B.G.: Davis, P.: Churcher, C.M.

submitted to the EMBL Data Library, August 1999
A-Reference number: 221840

A;Accession: T39268
A;Status: preliminary; translated from GB/EMBL/DDBT

A; Molecule type: DNA
A: Residues: 1-429 <LYN>

A; Cross-references: EMBL

C;Genetics:

A;Map position: 2

Percent Similarity:	Percent Identity:
51.327	24.779

alignement_block:
US-09-922-067-9

Align seq 1/1 to: T39269

200 A A T C C C C C C C C A A T C C C C C C C C C C C C C C C C C C C

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10 clear enDraC laTtuGucCluDrOI enDroVa] Cl uSotI enV= lI enUcl 26

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[illegible][illegible]

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Figure 1: Schematic representation of the experimental design. The diagram illustrates the sequence of events in the experiment. It shows a series of vertical bars representing stimuli, followed by a response (a vertical bar with a dot), and then a feedback signal (a vertical bar with a dot). The sequence is repeated for multiple trials, with the subject's response and the feedback signal being recorded for each trial. The diagram is labeled 'Figure 1' and 'Schematic representation of the experimental design'.

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[illegible][illegible][illegible]

88 euA gA tA pHeA tA sEr gL yLeu tIn r As nI Leu A tA Leu P rO tO t

C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: D83408
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizioch, S.D.; Warriner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.K.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337
 A:Accession: D83408
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-546 <STO>
 A:Cross-references: GB:AE004616; GB:AE004091; NID:9947890; PIDN:AAG05295.1; GSPDB:GN003
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1907

alignment_scores:
 Quality: 162.50 Length: 437
 Ratio: 0.781 Gaps: 18
 Percent Similarity: 47.597 Percent Identity: 21.968

alignment_block:
 US-09-922-067-9 x D83408 ..

Align seg 1/1 to: D83408 from: 1 to: 546

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167 GTACTGATGCTGCTGCAAGC.....TTTGGCCAAACTAAATCCC 207
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 ValLeuLeuAlaLeuAlaLeuLeuLeuPheProValAlaProLeuPr 105
208 CCGGGGAAATGGGCTTATTCCTGCTGTTGTTACAGACTTATGTTGATC 257
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
105 oAlaProSerGlyProTyrAlaValGlyValArgAspPheGluLeuAspA 122
258 ACACATAAAG.....GGCACC..... 274
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 sProSerArgProGlyLeuLeuGlyThrProAlaGlyGlnProArgArg 138
275 ...TTCTTGGCTTTATATTCATCCCAAGATAATGATCCCTGACAC 321
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 LeuLeuValArgAlaTrpTyrProAlaArg.....ProIl 150
322 CCCTTGGATCCCAATAAGAAATATTT..... 349
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
150 eAlaGlyAlaAlaProArgHisTyrPheAspProGlyGluAlaArgSert 167
350 ....TGGGCTTAGCAAAATTTCTTGGACACACACTGGCTTATGGGCAAC 394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
167 hrAlaArgGlyPheGlyGluLeuGlyPheProProLeuLeuThrTyr 183
395 ATTTTGGAGTTACTCTTGGTTCAATGACACTCTGCTGCAAACTGGAATTC 444
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 LeuLysHisLeuArgThrAsnSerTyrPro.....AspAl 195
445 CCCTCTGAGG...CCTGCTGAAATATCCACTTGTCTTTTCTCATG 491
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
195 aProLeuArgAspAspSerAlaArgLeuProValPheTyrSerHisG 212
492 GTCTTGGGCTTACAGGACACTTATCTGCTATGTCATTCGACCTGGCA 541
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
212 ltyrSerAlaPheAlaGlyGlyAsnTrpThrLeuMetGluLeuAla 228
542 TCTCATGGGTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATC 591
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
229 SerHisGlyTyrAlaValTyrAlaIleGlnHisSerGly..... 241
592 TGCAACTTACTATTTCAGGACCAATCTGCTGCCAAATAGGGGACAGT 641
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
242 .....AspAlaSerProThrArgLeuProAspGlyT 252

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642 CTGGCTCTACTCTAGAACCCCTGAAACAGAGAGAGACACATATACGA 691
|||:|||||:|||||:|||||:|||||:|||||:|||||:
252 hrLeuLeuProMetArgProGlyLeuValGluHisLeuArgAlaAla 268
692 AATGACGAGGTACGGCAAGAGCAAGAA.....TGTTCACAGCTCT 735
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 HisAspGlyLeuProGlnAlaMetArgGlnGlyTyrValSerAspAsp 285
736 CAGTCTGATCTTCTGAC.....ATTGATCATCGAAAGC 767
|||:|||||:|||||:|||||:|||||:|||||:|||||:
285 uAspGlnArgLeuAspGlyGlnLeuHisThrAlaLeuAspLeuProAlaP 302
768 CAGTGAAGAAATGCAATTAAG..... 793
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
302 roAlaAsnArgAlaValAsnLeuSerAlaProValTrpLeuAlaAspArg 318
794 ...TTTGATATGGAACAACTGAGGACTCTATTGATAGGGGAAATAATAC 840
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 LeuPheValHisAspArgLeuGlnAlaGlyGluValProAspArgValAl 335
841 A.....GTAATTGGACATT 854
|:|||||:|||||:|||||:|||||:|||||:|||||:
335 aAspLeuValAlaAlaSerAspPheAlaHisThrGlyGluMetGlyMets 352
855 CTTTGGTGGACCAAGGTTTATTCAGACTCTTAGTGAAGATCAGACATTC 904
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
352 erPheGlyGlySerThrThrGlyAlaValCysMetValAspArgArgCys 368
905 AGATCTGCTATGCTGATGATGATGATGATGATGATGATGATGATGAT 954
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 AlaAlaAlaValAsnLeuAspGlyGlyAspPheAspPheAla...ProPh 384
955 ATATTCCAGAAATCTCAGCCCTCTTTTATCAACTCTGAAATATTTCC 1004
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
384 eAspSerAspPheProAlaProLeuLeuMetLeuHisAlaAspLeu.... 399
1005 AATATCTGCTATATATATATATATATATATATATATATATATATAT 1054
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
400 .....GlyAsnPheTyrArgLeuPheGlyIleGluProProAlaArg 413
1055 GAAAGAAAGATG..... 1066
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
414 ProArgSerPheAsnAspPheSerTyrGluArgPheGluHisAlaGlyL 430
1067 .....ATTACAATCAGGGTTTCAGTCCACAGAAAT 1097
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
430 nArgGlnAspIleHisArgLeuValLeuArgAspSerAlaHisAlaGlyL 447
1098 TTGCTGACTTCTACTTTTGGCACTGGCAAAATAATTTGACACATCTCAA 1147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
447 euThrAsp.....AsnProLeuPheIleArgArgProLeuArg 459
1148 .....TTAAGGGAGACATAGATTCAAAATGACGCTATTGATCTTAGCA 1191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
460 AspGlyLeuLeuGlySerAlaProThrGluValLeuIleGlnAlaProAs 476
1192 CAAAGCTTCTTACTTCTTCAAAAGCAATTTA...GGACTTCAATAAG 1238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
476 nAlaLeuValLeuGlyPhePheAspHisTyrLeuArgGlyArgAlaAsnA 493
1239 ATTTTTCATCAG 1249
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 spPheProGln 496

```

seq_name: pir2:T36311

seq_documentation_block:

probable lipase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36311

R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
 submitted to the EMBL Data Library, March 1999

[illegible]

444 CCCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGTTGTTTTCTCATGGT 493

444 CCCCTCTGAGGCCCTGGT

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105 ..... |||||:|||| |||
494 CTTGGGCAATTCAGACACTTTATTCTGCTATTGGCATTGACCTGGCATC 543
   :|||:||||: :|||:|||||
111 PheThrAlaTyrGlnSerSerIleAlaTrpLeuGlyProArgLeuAlaIle 127
   :|||:||||: :|||:|||||
544 TCATGGGTTTATAGTGTCTGCTGTAGAACACAGACATAGATCTGCATCTG 593
   :|||:||||: :|||:||||:
127 rGlnGlyPheValValPheThrIleAspThrAsn..... 138
594 CAACTTACTATTTCAGAGGCAATCTCTGCAGAAATAGGGGACAAGTCT 643
138 .....
644 TGGCTCTACCTTAGAACCTTGAACCAAGAGGAGGAGACACATATACGAAA 693
   :|||:||||: :|||:||||:
139 .....ThrThrLeuAspGlnProAsp..... 145
694 TGAGCAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGA 743
145 .....
744 TTCTTGACATTGATCATGGAAGCCAGTGAAGATGCATTAGATTAAAG 793
146 .....SerArgGlyArgGlnLeuSerAlaLeuAspTyrLeu 158
794 TTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAGAAATAGCAGT 843
   :|||:||||: :|||:||||:
159 ThrGlnArgSerSerValArgThrArgValAspAlaThrArgLeuGlyVa 175
844 AATTGACATCTTTTGGTGGACACGGTTATTTCAGACTCTTAGTGAAG 893
   :|||:||||: :|||:||||:
175 lMetGlyHisSerMetGlyGlyGlySerLeuGluAlaAlaLysSerA 192
894 ATCAGAGATTCAGATGTGTATTGCTCCTGCATGATGCTTTCACCTG 943
   :|||:||||: :|||:||||:
192 rgThrSerLeuLysAlaAlaIleProLeuThrGlyTrpAsn..... 205
944 GGTGATGAAGTATTCAGAAATTCCTCAGCCCTCTTTTATCAACTC 993
   :|||:||||: :|||:||||:
206 ThrAspLysThrTrpProGluLeuArgThrProThrLeuValGlyAl 222
994 TGA.....TATT 1001
222 aAspGlyAspThrValAlaProValAlaThrHisSerLysProPheTyrG 239
1002 TCCAAATATCCTGCTAATATCATATAAAATCAAAATGCTTACTCACCTGAT 1051
   :|||:||||: :|||:||||:
239 luSerLeuProGlySerLeu..... 245
1052 AAGAAAGAAGATGATTACAAATCAGGGGTTTCAGTCCAC.....CAGAA 1095
   :|||:||||: :|||:||||:
246 ...AspLysAlaTyrLeuGluLeuArgGlyAlaSerHisPheThrProAs 261
1096 TTTTGTCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCA 1145
   :|||:||||: :|||:||||:
261 nThrSerAspThrThrIleAla..... 268
1146 AATTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTACCAACAAA 1195
269 .....Lys 269
1196 GCTTCATTAGCATCTTACAAAAGCAATTTAGGACTTTCATAAGATTTTGA 1245
   :|||:||||: :|||:||||:
270 TyrSerIleSerTrpLeuLysArgPheIleAspSerAspThrArgTyrGl 286
1246 TCAGTGGGACTGCTGTGATT 1264
286 uGlnPheLeuCysProIle 292

```

seq_name: p1r2:S75452

```

seq_documentation_block:
hypothetical protein slr1506 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75452
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, Y.; Miyajima,
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synech.
S.

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A:Reference number: S74322; MUID:97061201

A:Accession: S75452

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-622 <KAN>

A:Cross-references: EMBL:D90911; GB:AB001339; NID:q1653083; PIDN:BAAL8013.1; PID:

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

alignment_scores:

```

Quality: 119.00 Length: 351
Ratio: 0.708 Gaps: 16
Percent Similarity: 47.863 Percent Identity: 21.368

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alignment_block:

US-09-922-067-9 x S75452 ..

Align seg 1/1 to: S75452 from: 1 to: 622

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385 TATGGCAACATTTTGAGGTTACTCTTGGTTCAATGACACTCTCGCAA 434
   ||||| :||| :|||:|||||:||||| :|||
257 TyrGlyValAlaProLysGluThrTrpTrpLeuAsnAspGlnSerArgAs 273
435 ACTGGAATTC.....CCTCTGAGGCGCTGGTCAA... 463
   :|||:||||: ||||| :|||
273 nArgArgPheTyrValAspValTyrArgProGln.ArgTrpLysGluGly 289
464 AAATATCCACTTGTCTTTTTCATGCTCTTGGGCGCATTCAGGACACT 513
   ||| :|||:|||||:|||||:||||| :|||
290 LysThrProValLeuValPheSerHisGlyLeuAlaSerArgProGluAs 306
514 TTATTCTGCTATTGGCATTCGCTGTCATCTGGTTTATGTTATCTGCTG 563
   :|||:||||: :|||:|||||:|||||:|||||
306 pPheAspAsnAlaAlaGluLysMetAlaSerTyrGlyPheValAlaAla 323
564 CTGTAGAACAC.....AGAGAT 580
   :|||:||||:
323 euProGlnHisProGlySerAspIleLeuGlnAlaLeuLeuAsn 339
581 AGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTCTGCAGAAAT 630
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340 ArgThrSerArgGlnGlyTyrTyr.....ProThrGluPh 351
631 AGGGGACAAAGTCTTGGCTCTACCTTAGAACCTGAAACAAGAGGAGGAGA 680
   :||| :||| :|||:||||:
351 eileAsp.....ArgProLysAspIleS 359
681 CACATATACGAATAGCAGAGGTACGGCAAGAGCAAAAGAATGTTCCCAA 730
   :|||:||||: :|||:|||||:||||| :|||
359 erTyrValIleAspGluLeuGluArgAsnAlaSerGluPheGlyAsp 375
731 GCTCTCAGTCTGATTTCTTGACATTCATCATGGAACCCAGTGAAGAATGC 780
   :|||:||||:
376 ArgLeuAsnLeu..... 379
781 ATTAGATTAAAGTTTGATATGAACAACCTGAAGGACTCTATTGATAGG 830
380 .....T 380
831 AAAAAATAGCAGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAG 880
   :|||:||||: |||||:|||||:||||| :|||
380 hrGlnValGlyValGlyGlyHisSerPheGlyGlyTyrGlyAlaLeuAla 396

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881 ACTCTTAGTGAAGATCAGACATTCAGATGTGGTATTGCGCTGGATGCATG 930
   :::: ||| :::: ||| ||
397 Val .....AlaGlyAlaThrIleAsp...Tr 404
   :::: ||| :::: ||| ||
931 GATGTTTCCACTGGGTGAT...GAAGTATATCCAGAATTCTCGAGCCCC 977
   ||| ||| :::: ||| ||
404 pAspPheLeuLysSerGluCysArgIleGlyGlnGlyValProAsnThrA 421
   :::: ||| :::: ||| ||
978 TCTTTTATCACTCTGAATATTCCAATATCTCTGCTTAATATCATATAA 1027
   :::: ||| :::: ||| ||
421 laLeuLeuLeuGlnCysAspAlaLeuThrLeuProArgSerAspTyrAsp 437
   :::: ||| :::: ||| ||
1028 ATGAAAAAATGCTACTACCTCGATGATAAGAAAGAGATGATTACATCAG 1077
   :::: ||| :::: ||| ||
438 Phe .....ArgAspProArgValAlaValIle 447
   :::: ||| :::: ||| ||
1078 GGGTTCAGTCCACGAGAAATTTTGTGACTTC...ACTTTTGCAGTGGCA 1124
   :::: ||| :::: ||| ||
447 uAlaAlaAsnProValAsnSerAlaIlePheGlyValSerGlyLeuHisL 464
   :::: ||| :::: ||| ||
1125 AAATAATTGGACATGCTCAANTTAAGGGAGACATAGATCAANTGCA 1174
   :::: ||| :::: ||| ||
464 ySValThrValProValLeuLeuGlyGlySerTyrAspProAlaThr 480
   :::: ||| :::: ||| ||
1175 GCTATTGATCTTAGCAACAAAGCTTCA.....TTAGCATTTCTTACA 1215
   :::: ||| :::: ||| ||
481 PropheValLeuGluGlnAlaArgSerPheProArgLeuAlaSerArgAs 497
   :::: ||| :::: ||| ||
1216 AAAGCATTTAGGACTT.....CATAAAGATTTTGTATCAT 1250
   :::: ||| :::: ||| ||
497 pLysTyrLeuThrLeuMetGluGlyGlnAlaHisValAspPheSerLysI 514
   :::: ||| :::: ||| ||
1251 GGGACTGCTTGAATCAAGAGATGATGAGATCTT..... 1285
   :::: ||| :::: ||| ||
514 leAspAlaAsnIleLysAsnValValGluSerValGluAlaValSerLeu 530
   :::: ||| :::: ||| ||
1286 ...ATTCCAGGGACCAAC...ATTACACACCAACCAATCAACACATCATGT 1329
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531 LysLeuProAspProAsnLeuLeuHisThrTyrGlySerAlaValMetVa 547
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1330 A 1330
   :
547 I 547

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seq_name: pir2:D75217

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seq_documentation_block:
probable 2-acetyl-1-alkylglycerophosph ocholine esterase PAB2176 - Pyrococcus abyssi (st
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: D75217
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75217
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <RAW>
A:Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CA849187.1; PID:e151508
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2176

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alignment_scores:
Quality: 112.00      Length: 299
Ratio: 0.889        Gaps: 13
Percent Similarity: 42.140      Percent Identity: 22.408

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alignment_block:
US-09-922-067-9 x D75217

```

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Align seg 1/1 to: D75217 from: 1 to: 286
206 CCCCGGGAAATGGGCTTATCCGTTGGTTGTACAGACTTAATGTTGA 255
   ||||| ||| :::: ||||| |||||
29 ProArgValGlyLysTrpThrPro.....LysAspLeuGlyPheAs 43
   :::: ||| :::: ||| ||
256 TCACACTAATAAGGCGACCTCTCTGGTGTATATATATCCATCCCAAGATA 305
   :::: ||| :::: ||| ||
43 pTyrGlu.....LysValGluPheLysSerArgAspG 54
   :::: ||| :::: ||| ||
306 ATGATCGCCTTGACACCCCTTGGATCCCAATAAAGAATATTTTGGGGT 355
   :::: ||| :::: ||| ||
54 lYlleThrLeuArgGlyTrpTrpIleAspGlnGlyLys..... 66
   :::: ||| :::: ||| ||
356 CTTAGCAAAATTTCTTGGACACACTGGCTTATGGCAACATTTTGGAGTT 405
   :::: ||| :::: ||| ||
67 .....AspGluThrValIleVa 72
   :::: ||| :::: ||| ||
406 ACTCTTTGTTCAATGACAACCTCTGCAAACTGGAATTCCTCTGAGGC 455
   ||| ||| :::: |||||
72 lLeuHisGly.....TyrThrAlaSerLysTrpAsn..... 82
   :::: ||| :::: ||| ||
456 CTGGTGAAAAATAT.....CCACTGTTGTTTTCATGCTCTTGGG 499
   ||| ||| :::: ||| ||
83 .....GluValTyrMetLysProAlaIleGluIleValAlaAsnLeuGly 97
   :::: ||| :::: ||| ||
500 GCATTTCAGGACACTTTATCTCTGATTGGCATTCGACCTGGCATCTCATGG 549
   :::: ||| :::: ||| ||
98 .....TyrAsnValLeuThrPheAspPheArgAlaHisG1 109
   :::: ||| :::: ||| ||
550 GTTATATAGTGTCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACT 599
   :::: ||| :::: ||| ||
109 y..... 109
   :::: ||| :::: ||| ||
600 ACTATTTCAAGGACCAATCTCTGCGAGAAATAGGGGACAGCTCTGGGTC 649
   :::: ||| :::: ||| ||
110 .....GluSerGluGlySerLysThrThrIleGlyAsp..... 120
   :::: ||| :::: ||| ||
650 TACCTTAGAACCCCTGAAACAAAGAGGAGGACACATATACGAAATGAGCA 699
   :::: ||| :::: ||| ||
120 ..... 120
   :::: ||| :::: ||| ||
700 GSTACGGCAAAGAGACAAAAGAATGTTCCCAAGCTCTCAGTCTGATTTTG 749
   :::: ||| :::: ||| ||
120 ..... 120
   :::: ||| :::: ||| ||
750 ACATTGATCATGGAACCCAGTGAAGATGCATTAGATTTAAAGTTTCAT 799
   :::: ||| :::: ||| ||
121 .....LysGluIleLeuAspLeuSerGlyAla 129
   :::: ||| :::: ||| ||
800 ATGGAACAACTGAAGGACTCTATTGATAGGGAAGAAATAGCAGTAATTTGG 849
   :::: ||| :::: ||| ||
130 lLeAspTrpLeuLeuSerAsnThrAsnThrLysLysIleAlaLeuIleG1 146
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850 ACATCTCTTTGGTGAGCAACGGTATTATTCAGACTCTTAGTGAAGATCAGA 899
   :::: ||| :::: ||| ||
146 yPheSerMetGlyAlaMetValThrIleArgAlaLeuAlaGluAspGluA 163
   :::: ||| :::: ||| ||
900 GATTTCAGATGTGTTATTCCTGATGCATGCATGATGTTTCCACTGGGTGAT 949
   :::: ||| :::: ||| ||
163 rgValCysCysGlyIleAlaAspSerProPheIleTyrIle.....Asp 177
   :::: ||| :::: ||| ||
950 GAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATCACTCTGTAATA 999
   :::: ||| :::: ||| ||
178 LysThrGlyAlaArgGlyLeuLys.....TyrPheAlaAsnLeuProG1 192
   :::: ||| :::: ||| ||
1000 TTTCCAATATCTCTCTAATATCATATAA...ATGAAAAAATGCTACTCAC 1046
   ||| ||||| ||||| ||| ||| ||| |||
192 uPheLeuTyrPro.....lLeIleLysProPheThrLysMetPheSerG 207
   :::: ||| :::: ||| ||
1047 CTGATAAAGAAAGAAAGATGATTACATCAAGGGGTTTCCATCCACCAG 1093
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572

C:\Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C:Accession: F71174
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Håkawa, Y.; Hino, Y.; Yamamoto, S.; Sekiguchi, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus furiosus
 A:Reference number: A71000; MUID:98344137
 A:Accession: F71174
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-622 <RAW>
 A:Cross-references: GB:AP000002; NID:93236129; PIDN:BAA29683.1; PID:g3257000
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0594

alignment_scores:
 Quality: 110.00 Length: 290
 Ratio: 0.932 Gaps: 14
 Percent Similarity: 40.690 Percent Identity: 20.345
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 Align seg 1/1 to: F71174 from: 1 to: 622

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344 TATTTTGGGGT.....CTTAGCAAAATTTCTGGACACAC 378
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287 TyrLeuTrpAspGlyGluValArgGluLeuAlaLys.....GlyLysHI 301
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379 CTGGCTTATGGGC.....AACATTTTGAGTTACTCTTTGGTT 416
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301 strPileMetGlyPheAspAlaAspGluArgGluLeuLysGluT 318
|||||
417 CAATGACAACTCTCCAAAC.....TGGAAATCC..... 445
|||
318 hrAlaThrArgProAlaGluLeuTyrLeuTrpAspGlyGluGluArgGln 334
|||||
445 ..... 445
335 LeuThrAspTyrAsnGlyLeuIlePheLysLysLeuLysThrPheGluPr 351
|||||
445 ..... 445
351 oArgHisPheArgPheLysSerIleAspLeuGluLeuAspGlyTrpTyrI 368
|||||
446 .....CCTCTAGGCGCTGTGAAAATATCCACTTGTCTTTTCT 487
|||||
368 LeLysProGluLeuLysGluGlyGluLysAlaProValIleValPheVal 384
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488 CATGCT.....CTTGGGCGCATTCAGGACACTTTATCTGCTATTGGCAT 531
|||||
385 HSLGlyGlyProLysGlyMetTyrGlyTyrPheLysTyrGluMetG1 401
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532 TGACCTGCATCTCATGGTTTATAGTTGCTGCTGTAGAACACACAGATA 581
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401 nLeuMetAlaSerLysGlyTyrIleValTyrValAsnProArgGlyLys 418
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418 eAsnGly.....TyrSerGluAsp..... 424
|||||
632 GGGGCAAGCTCTGCTCTACCTTAGAACCTTGAACAAAGAGGAGGAGAC 681
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425 .....PheAlaLeuArgValLeu.....GluArgth 433
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433 rGlyLeuGluAspPheGln..... 439
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732 CTCTCAGCTGATCTTGACATTTGATCGGAAGCCAGTGAAGAATGCA 781
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440 .....AspIleLeuAsnGly 444
782 TTAGATTTAAAGTTTATATGGAACAACCTGAAGACTCTATTGATAGGA 831
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445 IleGlu.....GluPheLeuArgLeuGluProGlnAlaAspArgG1 458
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832 AAAATAGCAGTAATTTGGACATTTCTTTTGGTGGAGCAACGGTTATTCAGA 881
|||||
458 uArgIleGlyIleThrGlyLeuSerTyrGlyGlyTyrMetThrAsnTrpA 475
|||||
882 CTCTTAGTCAAGATCAGATTCAGATGCGTATTGCC..... 919
|||||
475 lateuThrGlnSerAspLeuPheLysAlaGlyIleSerGluAsnGlyIle 491
|||||
920 .....CTGGATGCATGGATGTTT..... 937
|||||
492 SerTyrTrpLeuThrSerTyrAlaPheSerAspIleGlyLeuTrpPheAs 508
|||||
938 .....CCACTGGGTGATGAAGTATATATTCAGAA 965
|||||
508 pLysGluValIleGlyAspAsnProLeuGluAsnGluAsnTyrArgLysL 525
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966 TTCCTCAGCCCTCTTTT 985
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525 eu....SerProLeuPheTyr 530
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seq_name: pir2:T36421

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seq_documentation_block:
 hypothetical protein SCF34.22 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36421
 R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, September 1999
 A:Reference number: Z21606
 A:Accession: T36421
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Residues: 1-326 <SAU>
 A:Cross-references: EMBL:AL109974; PIDN:CAB53333.1; GSPDB:GN00070; SCOEDB:SCF34.22
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCF34.22

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 508 GACACTT.....TATCTGCTATTGGCATTCACCTGGCAT 542
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 60 nHisLeuSerSerLeuAspGlyTyrAlaProLeuAlaThrTyrTrpAlaA 77
 543 CTGATGGTTTATAGTTGCTGCTAGAACACACAGATAGATCTGCATCT 592
 : |||
 77 IaHSLGlyPheValIleGlnProThrHis..... 87
 593 GCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGCAAGTC 642
 87 87
 643 TTGGCTCTACCTTAGAACCTTGAACAAAGAGGAGGACACATATACGAA 692

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88 ...LeuSerSerArgThrLeuAlaLeuAspProGlyThrProGlyAlap 103
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693 ATGACAGGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTG 742
    |||:::|||||:::|||||:::|||||
103 roLeuPheTrpArgSerArgAlaGluAspMetThrArgValLeu..... 117
    :::::|||||:::
743 ATTCTTGACATTGATCATGGAAAGCCAGCTGAAGAATGCATTAGAT...TT 789
    :::::|||||:::
118 .....AspGlyLeuAspLeuLe 123
    .....
790 AAAGTTTGATATGGAACAACCTCAAGGACTCTATTGTAGTAGGAAAAAATAG 839
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123 uGluLysAlaValProGlnLeuSerGlyArgLeuAspArgSerArgVala 140
    .....
840 CAGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGT 889
    ||||| |||||||:::|||||:::
140 laValAlaGlyHisserMetGlyGlyHisThrAlaSerLeuLeuLeuGly 156
    .....
890 .....GAAGATCA 897
    .....
157 AlaArgLeuThrAspProAspAspGlyThrGluValAspLeuThrGluPr 173
    :::
898 GAGATTACAGATGTGGTATTGGCTGGATGCATGGATGTTTCCA..... 940
    ||||::: |||||||::: ||| |||
173 oArgIleGlyAlaGlyValLeuLeuAlaAla.....ProGlyArgG 187
    .....
941 .....CTGGGTGATGAAGTATATCCAGAATTCCTCAGGCCCTC 979
    |||:::|||||::: ::: |||
187 lyGlyAspAlaLeuSerGluSerAlaAlaGluSerMetPro..... 200
    .....
980 TTTTTCCTCAACTCTGAAATTTCCAAAT.....CTGCTCAATATCAT 1023
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201 PhePheLeuSerThrAspPheSerArgMetThrThrProAlaLeuValVa 217
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1024 A 1024
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217 i 217

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OM of: US-09-922-067-9 to: SwissProt_39:* out_format : pfs
Date: Mar 9, 2002 12:29 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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-Q/cgn2_1/USPTO_SPOOL/US09922067/runat_07032002_140446_9437/app_query.fasta_1.1439
-DB=SwissProt_39 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.000 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsu62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -MINLEN=0 -MAXLEN=2000000000
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Search information block:
Query: US-09-922-067-9
Query length: 1361
Database: SwissProt_39:*
Database sequences: 100059
Database length: 36664827
Search time (sec): 78.140000

score_list:	Sequence	Strd Orig	ZScore	EScore	Len	Documentation
	SwissProt_39:PAPA_HUMAN	2354.00	3570.52	7.5e-192	441	013093 h platelet-activating
	SwissProt_39:PAPA_BOVIN	1964.50	2977.71	7.8e-159	444	028017 b platelet-activating
	SwissProt_39:PAPA_CANFA	1935.50	2933.57	2.2e-156	444	028262 c platelet-activating
	SwissProt_39:PAPA_CAVPO	1572.50	2381.30	1.3e-125	436	070683 c platelet-activating
	SwissProt_39:PAPA_MOUSE	1515.50	2294.48	9.0e-121	440	060963 m platelet-activating
	SwissProt_39:PAPA_CHICK	1131.50	1710.45	3.2e-88	422	090678 g platelet-activating
	SwissProt_39:PA2_HUMAN	797.00	1202.03	7.1e-60	392	099487 homo sapiens (human)
	SwissProt_39:PA2_BOVIN	747.00	1125.94	1.2e-55	392	079106 bos taurus (bovine)
	SwissProt_39:PAPA_CAEEL	493.50	738.50	3.9e-34	476	022943 caenorhabditis elegans
	SwissProt_39:DAP1_YEAST	103.50	139.27	0.4710	931	033894 saccharomyces cerevis
	SwissProt_39:SYCP_CANAL	100.50	138.81	0.8091	575	078600 candida albicans (yea
	SwissProt_39:CLPE_CHEU	99.50	132.49	1.04	1010	042379 chlamydomonas eugame
	SwissProt_39:APY_ADEAE	99.00	136.72	1.08	562	050635 aedes aegypti (yellow)
	SwissProt_39:SYR_HELPJ	96.00	132.48	1.94	541	092mb9 helicobacter pylori j9
	SwissProt_39:CNRR_HUMAN	95.50	127.83	2.23	854	035913 homo sapiens (human)
	SwissProt_39:ESTP_DROME	95.00	130.91	2.35	544	018167 drosophila melanogast
	SwissProt_39:RS1_CHLTR	95.00	130.53	2.36	569	084100 chlamydia trachomatis
	SwissProt_39:JEN1_YEAST	95.00	129.85	2.38	616	036035 saccharomyces cerevis
	SwissProt_39:LECF_ALEAU	94.00	134.13	2.72	312	018891 aleuria aurantia (ora
	SwissProt_39:PRXV_ASCNO	94.00	129.19	2.87	557	081701 ascophyllum nodosum.
	SwissProt_39:RS1_CHLMU	94.00	128.99	2.87	570	038016 chlamydia muridarum.
	SwissProt_39:OPSD_CAMMA	93.00	132.94	3.29	300	018315 cambarus maculatus (c
	SwissProt_39:SN21_YEAST	92.50	132.26	3.63	297	003148 saccharomyces cerevis
	SwissProt_39:LIP_PSEAE	92.50	131.87	3.64	311	026876 pseudomonas aeruginosa
	SwissProt_39:LIP_PSEPE	92.50	131.87	3.64	311	026877 pseudomonas sp. (strai
	SwissProt_39:SYL1_SINY3	92.00	121.26	4.47	988	073505 synecocystis sp. (str
	SwissProt_39:TRMO_HELPJ	91.50	129.10	4.49	360	025893 helicobacter pylori (
	SwissProt_39:DPD4_RAT	91.50	122.66	4.81	767	014740 rattus norvegicus (rat
	SwissProt_39:MUS2_SINY3	91.50	122.07	4.84	822	073625 synecocystis sp. (str
	SwissProt_39:TRPE_HELPJ	90.50	124.78	5.62	500	025869 helicobacter pylori (
	SwissProt_39:ESTC_DROPS	90.00	123.29	6.25	545	025725 drosophila pseudoobs
	SwissProt_39:DHEA_HUMAN	90.00	123.09	6.26	558	049448 homo sapiens (human)
	SwissProt_39:LYTE_STRPN	90.00	121.68	6.36	658	0924p7 streptococcus pneumon
	SwissProt_39:TRPE_HELPJ	89.50	123.26	6.84	500	0923u5 helicobacter pylori (
	SwissProt_39:CP7A_PIG	89.50	123.24	6.84	501	046491 sus scrofa (pig). cytod
	SwissProt_39:NOS_RHOPR	89.50	115.99	7.40	1174	026240 rhodnius prolixus. na
	SwissProt_39:ESTB_DROPS	89.00	121.78	7.60	544	025727 drosophila pseudoobs
	SwissProt_39:DHEA_HUMAN	89.00	121.56	7.61	558	000367 homo sapiens (human)
	SwissProt_39:MYIA_RAT	89.00	115.51	8.13	1136	005096 rattus norvegicus (rat
	SwissProt_39:OPSD_CAMLU	88.50	126.06	7.93	301	016017 cambarus ludovicianus

SwissProt_39:IDH_ECOLI	+	88.50	123.30	8.17	416	008200 escherichia coli.
SwissProt_39:SYI_STAAR	+	88.50	116.57	8.79	917	041972 staphylococcus aur
SwissProt_39:MTR4_YEAST	+	88.50	115.23	8.92	1073	047047 saccharomyces ce
SwissProt_39:OPSD_ORCVI	+	88.00	125.30	8.74	301	016019 orconectes virili
SwissProt_39:TWFI_YEAST	+	88.00	124.47	8.82	332	053250 saccharomyces cer
seq_name: SwissProt_39:PAPA_HUMAN						
seq_documentation_block:						
ID	PAPA_HUMAN	STANDARD;	PRT;	441	AA.	
AC	Q13093;	Q15692;				
DT	01-NOV-1997	(Rel. 35, Created)				
DT	01-NOV-1997	(Rel. 35, Last sequence update)				
DT	20-AUG-2001	(Rel. 40, Last annotation update)				
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)					
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED					
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE					
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).					
GN	PLA2G7 OR PAFAH.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
[1]	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.					
RN	TISSUE=Myeloid;					
RC	MEDLINE=95214779; PubMed=7700381;					
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,					
RA	Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,					
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;					
RT	"Anti-inflammatory properties of a platelet-activating factor					
RT	acetylhydrolase.";					
RL	Nature 374:549-553(1995).					
[2]	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
RP	TISSUE=Lymphoma;					
RC	MEDLINE=96197208; PubMed=8624782;					
RA	Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,					
RA	Moore K., Gloger I.S., Macphie C.H.;					
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-					
RT	associated, serine-dependent phospholipase involved in the oxidative					
RT	modification of low-density lipoproteins.";					
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).					
[3]	MUTAGENESIS.					
RP	MEDLINE=96029630; PubMed=7592717;					
RA	Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,					
RA	Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,					
RA	Gray P.W.;					
RT	"Plasma platelet-activating factor acetylhydrolase is a secreted					
RT	phospholipase A2 with a catalytic triad.";					
RL	J. Biol. Chem. 270:25481-25487(1995).					
[4]	VARIANT PHE-279.					
RP	MEDLINE=96259525; PubMed=8675689;					
RA	Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,					
RA	Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,					
RA	McIntyre T.M., Gray P.W., Prescott S.M.;					
RT	"Platelet-activating factor acetylhydrolase deficiency. A missense					
RT	mutation near the active site of an anti-inflammatory					
RT	phospholipase.";					
RL	J. Clin. Invest. 97:2784-2791(1996).					
[5]	VARIANT PHE-279.					
RP	MEDLINE=98430412; PubMed=9759612;					
RA	Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,					
RA	Yoshimizu N., Fukushi K., Satoh K.;					
RT	"A mutation in plasma platelet-activating factor acetylhydrolase					
RT	(Val279phe) is a genetic risk factor for cerebral hemorrhage but not					
RT	for hypertension.";					
RL	Thromb. Haemost. 80:372-375(1998).					
CC	-1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)					
CC	BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY					

CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H₂O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -|- TISSUE SPECIFICITY: PLASMA.
 CC -|- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
 CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
 CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
 CC RESPONSES.
 CC -|- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U20157; AAC50126.1; -;
 CC EMBL; U24577; AAB04170.1; -;
 CC MIM; 601690; -;
 CC InterPro; IPR000379; Est_lip_thioest_actsite.
 CC InterPro; IPR000734; Lipase.
 CC PROSITE; PS00120; LIPASE_SER; 1.
 CC Hydrolase; Lipid degradation; Glycoprotein; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 441
 CC
 CC PLATELET-ACTIVATING FACTOR
 CC ACETYLDHIDROLASE.
 CC CHARGE RELAY SYSTEM.
 CC CHARGE RELAY SYSTEM.
 CC CHARGE RELAY SYSTEM.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .).
 CC V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
 CC PROTEIN).
 CC /FTID=VAR_004268.
 CC
 CC S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 CC S->A: LOSS OF ACTIVITY.
 CC D->A: ALMOST NO ACTIVITY.
 CC D->N: DIMINISHED ACTIVITY.
 CC D->N: LOSS OF ACTIVITY.
 CC D->N: LOSS OF ACTIVITY.
 CC D->A: NO CHANGE IN ACTIVITY.
 CC D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
 CC H->A: LOSS OF ACTIVITY.
 CC V -> A (IN REF. 2).
 CC
 CC SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

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Quality: 2354.00 Length: 441
 Ratio: 5.338 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.773

alignment_block:

US-09-922-067-9 x PAPA_HUMAN ..

Align seg 1/1 to: PAPA_HUMAN from: 1 to: 441

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 AC Q28017;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
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 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 OC Bovidae; Bovinae; Bos.
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 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad."
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -|- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -|- TISSUE SPECIFICITY: PLASMA.
 CC -|- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, LACTAL, ETC.).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC EMBL; U34247; AAC48483.1; -

DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR InterPro: IPR000734; Lipase.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolase; lipid degradation; Glycoprotein; Signal.
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alignment_block:
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ID PAFA_CANFA STANDARD; PRT; 444 AA.
AC Q28262;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACVLYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
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GN PLA2G7.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OX NCBI_TaxID=9615;
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RP SEQUENCE FROM N.A.
RC TISSUE=Spleen.
RX MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC
CC -!- TISSUE SPECIFICITY: PLASMA.
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CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.)
CC
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CC or send an email to license@isb-sib.ch).
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CC EMBL: U34246; AAC48484.1; -.
CC InterPro: IPR000379; Est_lip_thioest_actsite.
CC DR InterPro: IPR000734; Lipase.
CC DR PROSITE: PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
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DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
DE PLAZG7 OR PAFH.
GN Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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RN [1]
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RC STRAIN=HARTLEY; TISSUE=Liver;
RX MEDLINE=97103479; PubMed=8947850;
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
RA Yokoyama K., Setaka M., Nojima S.;
RT "Cloning, expression and characterization of plasma
RT platelet-activating factor-acetylhydrolase from guinea pig.";
RL J. Biochem. 120:838-844(1996).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; D67037; BAA11054.1; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
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DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 436 PLATELET-ACTIVATING FACTOR
 FT ACT_SITE 271 271 ACETYLHYDROLASE.
 FT ACT_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 436 AA; 49062 MW; C359D96E932FFE11 CRC64;

alignment_scores:

Quality: 1572.50 Length: 441
 Ratio: 4.022 Gaps: 2
 Percent Similarity: 88.662 Percent Identity: 66.213

alignment_block:

US-09-922-067-9 x PAFA_CAVPO

Align seg 1/1 to: PAFA_CAVPO from: 1 to: 436

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1 MetAlaProProLysLeuHisThrLeuPheCysLeuSerGlyPheLeuAl 17
88 TGTGTTTATCTCTTGTACTGGCAATACATAATCTGTTGCCATATGA 137
17 aLeuValHisProPheAspTrpArgAspLeuAspProValThrTrpIleG 34
138 AATCATCAGCATGGTGCACAAATACAACTACTGATGCTGCTGCAAGC 187
34 InSerSerValTrpIleGlnArgIleGlnSerGluLeuLeuIleThrSer 50
188 TTTGGCCAACTAAATCCCGGGGAAATGGCCCTTATCGCTGGTTG 237
51 PheGlyHisThrThrIleProLysGlyAsnGlyProTySerValGlyCy 67
238 TACAGACTTAATGTTGATACACACTAAATAAGGGCACTTCTTGGCTTAT 287
67 sThrAspLeuMetSerGlyTyThrAsnGlnSerSerPheLeuArgLeuT 84
288 ATTATCATCCCAAGATATGATCCCTTGACACCCCTTGGATCCCAAT 337
84 yTyProSerGlnAspAsnAspPheProAspAlaLeuTrpIleProAsn 100
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101 GluGlyTyPheGlnGlyLeuThrGluThrLeuGlyAlaSerSerPheLe 117
388 GGGCAACATTTTGGGTACTCTTGGTTGATCAATGCAACTCTCGCAAACT 437
117 uGlyLysLeuLeuLysLeuLeuTyGlySerValLysValProAlaLysT 134
438 GGAATTCCTCTGAGGCGCTGGTGAATAATATCCACTTGTGTTTCTTCT 487
134 rPasnSerProLeuLysThrGlyGlyLysTyProLeuIleIlePheSer 150
488 CATGGTCTTGGGCATTCAGGACACTTATTTCTGCTATTTGGCATGACT 537
151 HisGlyLeuGlyAlaPheArgSerIleTySerAlaIleGlyIleGlu 167
538 GGCATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGATAGATCTG 587
167 uAlaSerHisGlyPheIleValAlaAlaValGluHisArgAspGluSerA 184
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184 laAlaAlaThrTyTyPheGlnAspAlaProAlaAlaGluSerGlyAsn 200
638 AAGTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGGAGGAGACACATAT 687

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299 ProValGlyGluAspValHisSerLysIleProGlnProLeuPhePheI 315
988 CAACCTCTGAATATTTCCATATATCCTGCTAATATCATATAAATGAAAAAT 1037
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1038 GCTACTCACCTCATAAAGAAAGAAAGATGATTACAAATCAGGGGTTCAGTC 1087
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332 heTyGlnProGlnLysGluArgLysMetIleAlaValLysGlySerVal 348
1088 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTTGGACA 1137
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349 HisHisAsnPheValAspPheThrPheAlaThrGlyLysIleIleGlyGl 365
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382 leAsnLysAlaSerLeuAlaPheLeuGlnLysTyTyLeuGlyLeuAspLys 398
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seq_documentation_block:

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ID PAFA_MOUSE STANDARD; PRT; 440 AA.
AC Q60963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN PLAZG7 OR PAFAH.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
 RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
 RA Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
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 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC
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 CC -----
 DR EMBL: U34277; AAC52274.1; -
 DR MGD; MG1:1351327; Pla2g7.
 DR InterPro: IPR000379; Est_lip_thioest_actsite.
 DR ProSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 440
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 FT SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

alignment_scores:

Quality: 1515 50 Length: 442
 Ratio: 4.031 Gaps: 2
 Percent Similarity: 85.068 Percent Identity: 66.516

alignment_block:

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 66 sthrasplLeuMetPheGlyTyrGlyAsnGluSerValPheValArgLeu 83
 288 ATTATCCATCCCAAGATAATGATCGCTTGACACCTTGCACACCTTTGGATCCCAAT 337
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 938 CCNCTGGGTGATCAAGATATATCCAGAAATTCCTCAGCCCTCTTTTAT 987
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218 gAlaGlnGluCysLeuLysAlaLeuAsnLeuLeuLeuLysLeuSerG 235
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762 GAAAGCCAGTGAAGAATCATAGATTTAAAGTTTGTATATGGAACAATG 811
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235 lYgUluValMetAsnValLeuAsnSerAspPheAspTrpAsnHisLeu 251
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352 ThrPheValSerGlyGluIleIleGlyLysPhePheLysLeuLysGly 368
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402 LeuValAspGlyIleGlyProAsnValIleSerGlyThrAsnIleasp 417
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AC Q99487; O15458;
DT 30-MAY-2000 (Rel. 39, Created)
DE 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).
GN PAF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97115847; PubMed=8955149;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
RA Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
RT acetylhydrolase.";
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RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
RC TISSUE=Prostate;
RX MEDLINE=98161812; PubMed=9494101;
RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphie C.H.,
RA Moores K., Gloger I.S., Tew D.G.;
RT "Expression, purification and characterization of a human
RT serine-dependent phospholipase A2 with high specificity for oxidized
RT phospholipids and platelet activating factor.";
RL Biochem. J. 330:1309-1315(1998).
RN [3]
RP REVIEW.
RX MEDLINE=97364701; PubMed=9218411;
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RA "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -|- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
CC -|- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -|- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLUORIDE,
CC 3,4-DICHLOROISOCOUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DFP) AND
CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).
CC -|- SUBUNIT: MONOMER.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -|- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT
CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO
CC AMYGDALA AND FRONTAL CORTEX.
CC -|- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D87845; BAAL3468.1; -
DR EMBL: U89386; AAC39707.1; -
DR MIM: 602344; -
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR000734; Lipase.
DR PROSITE: PS00120; LIPASE_SER: 1.
KW Hydrolase; Lipid degradation.
FT ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 212 212 L -> F (IN REF. 2).
SQ SEQUENCE 392 AA; 44035 MW; 690FB7B6F5B68317 CRC64;
```

```
alignment_scores:
  Quality: 797.00
  Ratio: 2.919
  Percent Similarity: 72.800
  Length: 375
  Gaps: 6
  Percent Identity: 43.467
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alignment_block:

US-09-922-067-9 x PAF2_HUMAN ..

Align seg 1/1 to: PAF2_HUMAN from: 1 to: 392

206 CCCCGGGGAATGGCCCTTATTCGTTGTACAGACTTAATGTTGA 255

|||||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|

10 ProProValThrGlyProHisLeuValGlyCysGlyAspValMetGlu 26

256 TCACACTAATAAGGACCTCTCTTCGCTTTATATATATCCATCCCAAGATA 305

|||||: |||: |||:|||||: |||:|||||: |||:|||||: |||:|

26 yGlnAsnLeuGlnGlySerPhePheArgLeuPheThrProCysGlnLys 43

[illegible]


```

876 .....
1276 TGAAATCTTATTCAGGACCAACATTACACACCAATCAACATCA 1325
      |||||: |||||: .....
877 nLeuAsnLeuLeuGlyLeuThrAsnTyr.....AspMetHisIleP 891
1326 TGTTACAGAACTCTTCAGGAATAGAGAAATACAAT 1360
      ::::: |||||: .....
891 heProAspSerHisSerIleArgTyrHisAsn 902

seq_name: SwissProt_39:SYPC_CANAL

seq_documentation_block:
ID SYPC_CANAL STANDARD; PRT; 575 AA.
AC P78600;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLYL-TRNA SYNTHETASE, CYTOPLASMIC (BC 6.1.1.15) (PROLINE-- TRNA
DE LIGASE) (PROBS).
GN PRS.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 26555;
RX MEDLINE=98053570; PubMed=9392082;
RA Sentandreu M., Elorza M.V., Sentandreu R.;
RT "Isolation of a putative prolyl-trna synthetase (CapRS) gene from
RL Yeast 13:1375-1381(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA(PRO) -> AMP +
CC PYROPHOSPHATE + L-PROLYL-TRNA(PRO).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC
CC EMBL; U86341; AAC49876.1;
CC InterPro: IPR002106; AA_trna_ligase_II.
CC InterPro: IPR002314; trna-synt_2b.
CC Pfam: PF00587; trna-synt_2b; 1.
CC PRINTS: PR01046; TRNASYNTHPRO.
CC PROSITE: PS00179; AA_TRNA_LIGASE_II_1; 1.
CC PROSITE: PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 575 AA; 66209 MW; 477BE339CC4F6368 CRC64;

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alignment_scores:

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Quality: 100.50 Length: 262
Ratio: 0.824 Gaps: 9
Percent Similarity: 46.565 Percent Identity: 22.137

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alignment_block:

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US-09-922-067-9 x SYPC_CANAL

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Align seg 1/1 to: SYPC_CANAL from: 1 to: 575

```

```

245 TTAATCTTTGACACTAATAAGGACCTCTTGGCTTTATATATCC 294
      :: ||| ::|||: |||||:
258 IleTyrPheThrThrGluAspLysSerThrLeuIleCysAlaTyrTyrPr 274
      :: ||| ::|||: |||||:
295 ATCCCAAGATATGATGCGCTTACACCCCTTGGATCCCAATAAAA.... 340

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|||| | |||: |||||: |||||:
274 oSer.....AsnArgValLeuGluProLysPheIleGlnAsnGluIleP 289
341 .....GAATATTTTGGGCTCTTAGCAAAATTTCTTGAACA 376
      ::::: |||||: |||||:
289 roAspIleAspLeuAspSerIleAsnAspLeuSerGluPhe.....Asn 303
377 CACTGGCTTATGGCAACATTTTGGAGTTACTCTTTGGTTCAATGACAAC 426
      ::|||: |||||: |||||:
304 HisAspIleSerThrArgIleValArgIleMet..... 314
427 TCCTGCAAACTGGAAATTCCTCTGAGGCTTGGTGAATAATATCCACTTG 476
      ::||| ||| ::|||: |||||:
315 .....AspSerArgLeuSerSerArgSerLysPheProAspP 327
477 TTGTTTTCCTCATGCTCTTGGG...GCATTCAGGACACTTTATCTGCT 523
      ::|||: |||||: |||||: |||||:
327 heProIleSerAsnPheIleAsnArgSerLeuIleThrLeuThrAsp 343
524 ATTGGCATTGACCTGCGCATCTCATGGGTTTATAGTTGCTGCTGAACA 573
      ||| ||| |||||: |||||: |||||:
344 IleProIleValLeuAlaGlnGluGlyGluIleCysGlyHisCysGluG 360
574 CAGAGATAGATCTCATCTGCACTTACTATTCAAGGACCAACTCTGCTG 623
      : ||||| |||||
360 uGlyLysLeuSerAlaSer.....SerAlaI 369
624 CAGAAATAGGGACAAGTCTTGGCTCTACCTTAGAACCTCAACACAGAG 673
      ||||| |||||
369 leGluValGlyHisThrPheTyrIleu..... 377
674 GAGGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGAAATG 723
377 ..... 377
724 TTCCCAAGCTCAGTCTGATTTCTGACATTGATCGAAGCCAGTGA 773
      |||
378 .....GlyAspLysTyrS 382
774 AGAATGCATTAGATTTAAAGTTTGATATGCAACAACCTGAAGGACTATT 823
      ::||| |||||: |||||: |||||:
382 erLysProLeuAspLeuValAspValProThrSerAsnAsnSerIle 398
824 GATAGGAAAAAATAGCATAATTGGACATCTTTTGGTGGAGCAACGGT 873
      ::|||: |||||: |||||: |||||:
399 GluLysGlnArgIleMetMetGlyCysTyrGlyIleGlyIleSerArgII 415
874 TATTCAGACTCTTAGTAGAGATCAGAGATTGAGTGTGTTGCCCTGG 923
      ::||| ::|||: |||||: |||||: |||||:
415 eileAlaAlaIleAlaGluIleAsnArgAspGluLysGly.LeuLysTrp 431
924 ATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATTCCTCAG 973
      ::|||: |||||: |||||: |||||:
432 ProArgSerIleAlaProTyrGluValThrValVal...GluValSerIy 447
974 CCCCTCTTTTATCAACTCTGAATATTTCCAAT 1007
      : :: |||||: |||||: |||||:
447 sGlnLysGlnLeuLysAsnValAsnAspAsnAsn 458

seq_name: SwissProt_39:CLPP_CHLEU

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seq_documentation_block:

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ID CLPP_CHLEU STANDARD; PRT; 1010 AA.
AC P42379;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROBABLE CLPP-LIKE PROTEASE (EC 3.4.21.92) (ENDOPEPTIDASE CLP).
GN CLPP.
OS Chlamydomonas eugametos.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.

```


. 320 LysGlyTyrValAsnAlaGlnGlyAlaSerThrGlyProSerProArgTh 336
748 TGACATTGATCATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTG 797
336 rArgGlyMetHisAlaAspGlySerLeuAsnTyrLeuAspPheTyrSer 353
798 ATATGGAACAACCTGAAGGAC. 817
353 yrAsnAspSerTyrAsnAspPheLysThrAlaProArgGlyLysGlnAla 369
818TCTATGATAGGAAAAAATAGCAGTAATTTGGACA 852
370 GluArgAlaPheGlnGluGluSerLysLysValPheValIleIleAs 386
853 TTTCTTTTGTGGAGCA.ACGTTTATTCAGACTCTT. 886
386 nSerPheGlyGlySerValGlyAsnGlyIleThrValHisAspAlaLeuG 403
887AGTGAAGATCAGAGATTTCAGATGTGTATTTGCTCGAT 925
403 InPheIleLysAlaGlySerLeuThrLeuAlaLeuGlyValAlaIleSer 419
926 GCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAATTCCTCAGCC 975
420 AlaIleSerLeuAlaLeuAlaGlyGlyThr. 429
976 CTTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAAATC...A 1022
430IleGlyGluArgTyrValThrGluGlyCysHisValMetI 443
1023 TAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACA 1072
443 leHisGlnProGluCysLeuThrSerAsp.HisThrValLeuThr 457
1073 ATCAGGGGTTGAGTCCACAGAAATTTGCTGACTTTCACCTTTTGCACCTGG 1122
458 ThrArgGlyTyrIle.ProIleAlaAspValThr. 468
1123 CAAATAATTGCACATGCTCAATTAAGAGGAGACATAGATTCAATG 1172
469LeuAspAspLysVal 473
1173 CAGCTATTGATCTTAGCAACAAGCTTCATTAGCATTTCTTACAAAGCAT 1222
473 alAlaValLeuAspAsnAsnThrGlyGluMetSerTyr...GlnAsnPro 488
1223 TTAGGACTTCATAA...GATTTCGATCAGTGGGACTGCTTGTAT 1263
489 GlnLysValHisLysTyrAspTyrGluGlyProMetTyrGluValLysTh 505
1264 TGAAGGAGATGATGAGATCTTATTTCCA.GGGA 1295
505 rAlaGlyValAspLeuPheValThrProAsnHisArgMetTyrValAsnT 522
1296 CCAACATTAAACACCAACCAATCAACACATCATGCTTACAGAACTCTTCAGGA 1345
522 hrThrAsnAsnThrThrAsnGlnAsnTyrAsnLeuValGluAlaSerSer 538
1346 ATA 1348
539 Ile 539

seq_name: SwissProt_39:APY_AEDAE

seq_documentation_block:

ID APY_AEDAE STANDARD; PRT; 562 AA.
AC P50635;
DF 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE APYASE PRECURSOR (EC 3.6.1.5) (ATP-DIPHOSPHATASE) (ADENOSINE
DE DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE) (ALLERGEN AED A 1).

alignment_scores:

Quality: 99.00 Length: 401
Ratio: 0.553 Gaps: 19
Percent Similarity: 44.638 Percent Identity: 21.197

alignment_block:

US-09-922-067-9 x APY_AEDAE

Align seg 1/1 to: APY_AEDAE from: 1 to: 562

113 TACATAAATCTGTGTGCCATATGAATCATGAGCATGGTGCACAAATAAT 162
|||||
93 TyrLeuAsnAlaGlyAspAsnPheGlnGlyThrLeuTyrAsnLeuLe 109

GN APY.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Aedes;
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 308-331 AND 498-521.
RC STRAIN=ROCKEFELLER; TISSUE=Salivary gland;
RX MEDLINE=95148604; PubMed=7846038;
RA Champagne D.E., Smart C.T., Ribeiro J.M.C., James A.A.;
RT "The salivary gland-specific apyrase of the mosquito Aedes aegypti is
a member of the 5'-nucleotidase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:694-698(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ROCKEFELLER; TISSUE=Salivary gland;
RX MEDLINE=96101568; PubMed=7498420;
RA Smartt C.T., Kim A.P., Grossman G.L., James A.A.;
RT "The Apyrase gene of the vector mosquito, Aedes aegypti, is expressed
specifically in the adult female salivary glands.";
RL Exp. Parasitol. 81:239-248(1995).
CC -!- FUNCTION: FACILITATES HEMATOPHAGY BY PREVENTING ADP-DEPENDENT
PLATELET AGGREGATION IN THE HOST. MAY REDUCE PROBING TIME BY
FACILITATING THE SPEED OF LOCATING BLOOD.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O -> AMP + 2 PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: SALIVARY GLAND-SPECIFIC.
CC -!- DEVELOPMENTAL STAGE: NOT DETECTABLE IN FEMALES ON THE FIRST DAY
AFTER ECLOSION, BUT IS DETECTABLE ON THE SECOND DAY. IT IS
MAXIMALLY EXPRESSED BY DAY 4.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L12389; AAC37218.1; -;
CC EMBL; L41391; AAA99189.1; -;
CC InterPro; IPR002224; 5_nucleotidase.
CC InterPro; IPR000934; SerThr_phosphatse.
CC Pfam; PF01009; 5_nucleotidase_1.
CC PROSITE; PS00785; 5_NUCLEOTIDASE_1; 1.
CC PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
KW Hydrolase; Signal; Allergen.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 562 APYASE.
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 30 30 P -> A (IN REF. 2).
FT CONFLICT 358 358 G -> GG (IN REF. 2).
SQ SEQUENCE 562 AA; 62730 MW; F55FB7CF7AA4BFF6 CRC64;

SQ SEQUENCE 541 AA; 62158 MW; 81524A78BC125281 CRC64;

alignment_scores:

Quality: 96.00 Length: 294
Ratio: 0.686 Gaps: 15
Percent similarity: 47.619 Percent identity: 23.810

alignment_block:

US-09-922-067-9 x SYR_HELPJ ..

Align seg 1/1 to: SYR_HELPJ from: 1 to: 541

```

590 TCTGCAACTTAC.....TATTCAAGGACCAATCTGTCGAGAAAT 630
|||||.....|
182 SerValThrTyrProGluValPheTyrLysGlyGluTyrIleLeuGlu 198
|||||.....|
631 AGGGGACAAGTCTGG.....CTCTACCTTAGAACCCCTGAAACAAGAGG 674
|||||.....|
198 eAlaLysLysAlaHisAsnAspLeuGluProSerLeuPheLysGluAsnG 215
|||||.....|
675 AGGAGACATATACCAAAATGACGAGTACGGCAAGAGCAAAAGAATGT 724
|||||.....|
215 luGluThrIlelle.....GluValLeuSerAspTyrAlaLysAspLeu 229
|||||.....|
725 TCCCAAGCTCTCAGTCTGATCTTGCATTGATGATGGAAGCCAGTCAA 774
|||||.....|
230 .....MetLeuLeuGluIle.....LysGlyAsnLe 238
|||||.....|
775 GAATGATTAGATTAAAGTTTGTAT.....ATGG 803
|||||.....|
238 uAspAlaLeuAspIleHisPheAspSerTyrAlaSerGluLysGluValP 255
|||||.....|
804 AACAACTGAAGCACTATT...GATAGG...CAAAATAAGCAGTAATT 847
|||||.....|
255 heLysHisLysAspAlaValPheAspArgLeuGluLysAlaAsnAlaLeu 271
|||||.....|
848 GGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCA 897
|||||.....|
272 TyrGluLysAspSerLysThrPrlPheLysSerSerLeuTyrGlnAspG 288
|||||.....|
898 GAGATTCAAGATGCTGATTGCTCCCTGGAT...GCATGGATGTTTCCACTG 944
|||||.....|
288 uSerAspArgValLeuIleLysGluAspLysSerTyrThrTyrLeuAlaG 305
|||||.....|
945 GTGATGAAGTATATCCAGAATTCTCTCCGCCCTCTTTTTCATCACTCT 994
|||||.....|
305 lYAspIleValTyr.....HisAsp 311
|||||.....|
995 GAATATTCCAAATATCTGCTTAATATCATATAAAATGAAAAATGCTACTC 1044
|||||.....|
312 GluLysPheGln..... 315
|||||.....|
1045 ACCTGATAAAGAAAGAGATGATTACATCAGGGGTTTCAGTCCACCAGA 1094
|||||.....|
316 .....GlnAsnTyrThrLysTyrIleAsnIlePrlGlyAlaAspHisG 331
|||||.....|
1095 ATTTTGTCTGACTTCATCTTTTGCACATGGCAAAATAATTTGGACAC..... 1138
|||||.....|
331 lYThrIleAlaArgValLysAlaSerLeuGluPheLysGlyTyrAspSer 347
|||||.....|
1139 .....ATGCTCAAATTTAAAGGGAGACAT 1161
|||||.....|
348 SerLysLeuGluValLeuLeuAlaGlnMetValArgLeuLeuLysAsp... 363
|||||.....|
1162 AGATTCAAATGACGCTATTGCTATTCATCAACAAGCTTCA..... 1201
|||||.....|
364 .....AsnGluProTyrLysMetSerLysArgAlaGlyAsnPheIleL 378
|||||.....|
1202 .....TTAGCA 1207
|||||.....|
378 euIleLysAspValIleAspValGlyLysAspAlaLeuArgPheIle 394
|||||.....|

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1208 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTG 1257
|||||.....|
395 lLeuSerLysArgLeuAspThrHisLeuGluPheAspVal...AsnTh 410
|||||.....|
1258 CTTGATTGAAGGAGATGATGAGAAATCTTATCCAGGCGCAACATTAACA 1307
|||||.....|
410 rLeuLysLysGlnAspSerSerAsnProIleTyrTyrIleHisTyrAlaA 427
|||||.....|
1308 CAACCAATCAACACATCATCTTTACAGAACTCT 1339
|||||.....|
427 snSerArgIleHisThrMetLeuGluLysSer 437
|||||.....|

```

seq_name: SwissProt_39:CNRB_HUMAN

seq_documentation_block:

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ID CNRB_HUMAN STANDARD; PRT; 854 AA.
AC P35913;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ROD CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT
DE (EC 3.1.4.17) (GMP-PDE BETA).
GN PDE6B OR PDEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93351644; PubMed=8394243;
RA Kramtsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
RA Terpugov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
RT Structural studies of its cDNA and gene.";
RL FEBS Lett. 327:275-278(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93244036; PubMed=1338685;
RA Kramtsov N.V., Feshchenko E.A., Suslova V.A., Terpugov B.E.,
RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
RT phosphodiesterase from human retina.";
RL Bioorg. Khim. 18:1551-1554(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=92347868; PubMed=1322354;
RA Collins C., Hutchinson G., Kowbel D., Riess O., Weber B., Hayden M.R.;
RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase:
RT complete retinal cDNA sequence and evidence for expression in brain.";
RL Genomics 13:698-704(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92066478; PubMed=1720239;
RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
RA Andrew S., Schappert K., Hayden M.R.;
RT "Genomic organization and complete sequence of the human gene encoding
RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
RT 4p16.3.";
RL Nucleic Acids Res. 19:6263-6268(1991).
RN [5]
RP VARIANT ADP TYR-557.
RX MEDLINE=93350628; PubMed=8394174;
RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
RT "Recessive mutations in the gene encoding the beta-subunit of rod
RT phosphodiesterase in patients with retinitis pigmentosa.";
RL Nat. Genet. 4:130-134(1993).
RN [6]
RP VARIANT CSNB3 ASN-258.
RX MEDLINE=94355978; PubMed=8075643;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;

```

RT "Heterozygous missense mutation in the rod cGMP phosphodiesterase
 RL beta-subunit gene in autosomal dominant stationary night blindness."; [7]
 RN Nat. Genet. 7:64-68(1994).
 RP ERRATUM.
 RX MEDLINE=95038845; PubMed=7951329;
 RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
 RL Nat. Genet. 7:551-551(1994).
 RN [8]
 RP VARIANT ARRP ASP-576.
 RX MEDLINE=96129294; PubMed=8595886;
 RA Danciger M., Blaney J., Zhao D.Y., Zhao D.Y., Heckenlively J.R.,
 RA Jacobson S.G., Farber D.B.;
 RL "Mutations in the PDE6B gene in autosomal recessive retinitis
 pigmentosa.";
 RN Genomics 30:1-7(1995).
 RP [9]
 RX VARIANTS ADP LYS-166; HIS-212 AND HIS-228.
 RA MEDLINE=96273603; PubMed=8698075;
 RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J.,
 RA Jacobson S.G., Heckenlively J.H., Farber D.B.;
 RL "Screening of the PDE6B gene in patients with autosomal dominant
 retinitis pigmentosa.";
 RN Exp. Eye Res. 62:149-154(1996).
 RP [10]
 RX VARIANT ARRP ARG-699.
 RA MEDLINE=96140746; PubMed=8557257;
 RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
 RA Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,
 RA Baiget M.;
 RL "A novel mutation in exon 17 of the beta-subunit of rod
 phosphodiesterase in two RP sisters of a consanguineous family.";
 RN Hum. Genet. 97:35-38(1996).
 RP [11]
 RX VARIANT ARRP GLN-552.
 RA MEDLINE=97114306; PubMed=8956055;
 RA Valverde D., Baiget M., Seminago R., del Rio E., Garcia-Sandoval B.,
 RA del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.;
 RL "Identification of a novel R552Q mutation in exon 13 of the
 beta-subunit of rod phosphodiesterase gene in a Spanish family with
 autosomal recessive retinitis pigmentosa.";
 RN Hum. Mutat. 8:393-394(1996).
 RP [12]
 RX VARIANT ARRP ASN-535.
 RA MEDLINE=98205225; PubMed=9543643;
 RA Saga M., Mashima Y., Akao K., Kudoh J., Oguchi Y., Shimizu N.;
 RL "A novel homozygous Ile35Asn mutation in the rod cGMP
 phosphodiesterase beta-subunit gene in two brothers of a Japanese
 family with autosomal recessive retinitis pigmentosa.";
 RN Curr. Eye Res. 17:332-335(1998).
 CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
 TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
 FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
 CC -!- CATALYTIC ACTIVITY: GUANOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 GUANOSINE 5'-PHOSPHATE.
 CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
 BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF RETINITIS PIGMENTOSA
 (RP). RP IS A GROUP OF HUMAN DISEASES THAT LEADS TO DEGENERATION
 OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
 VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISUAL FIELD; AS THEIR
 CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISUAL FIELD
 AND EVENTUALLY CENTRAL VISION AS WELL. RP MAY OCCUR WITH AUTOSOMAL
 RECESSIVE (20-25% OF CASES; ARRP) AUTOSOMAL DOMINANT (15-20% OF
 CASES; ADP) OR X-LINKED (10-15% OF CASES; XRP) INHERITANCE.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF CONGENITAL STATIONARY
 NIGHT BLINDNESS (CSNB3).
 CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 FAMILY.
 CC -!- DATABASE: NAMP-Mutations of the PDE6A/B/G genes;
 CC NOTE-Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/pdemut.htm".

CC ----- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S41458; AAB22690.1; -
 DR EMBL: X66142; CAA46932.1; -
 DR EMBL: X62692; CAA44569.1; -
 DR EMBL: X62693; CAA44569.1; JOINED.
 DR EMBL: X62694; CAA44569.1; JOINED.
 DR EMBL: X62695; CAA44569.1; JOINED.
 DR PIR: A42828; A42828.
 DR PIR: S34590; S34590.
 DR MIM: 180072; -
 DR MIM: 268000; -
 DR MIM: 163500; -
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003607; HDC.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF01590; GAF; 2.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00065; GAF; 2.
 DR SMART: SM00471; HDC; 1.
 DR PROSITE: PS00136; PDEASE_I; 1.
 DR Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Membrane;
 KW Retinitis pigmentosa; Disease mutation.
 FT CHAIN 1 851
 FT PROPEP 852 854
 FT LIPID 851 851
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386 etProIleValAsnLysLysGluGluLeuValGlyValAlaThrPheTyr 402
701 GTACGGCAAGAGCAAAAGAATTTCCCAAGCTCTCAGTCTGATCTTTGA 750
403 AsnArgLysAspGlyLysProPheAspGluGlnAspGluValLeuMetG 419
751 C.....ATTG 755
419 userLeuThrGlnPheLeuGlyTrpSerValMetAsnThrAspThrTyrA 436
756 ATCATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGATATGCAA 805
436 sPLysMetAsnLysLeuGluAsnArgLysAspIleAlaGlnAspMetVal 452
806 CAACTGAAGGACTCTATTGATAGGCAAAAAAATAGCAATAATGGACATTC 855
453 LeuTyrHisValLysCysAspArgAspGluIleGlnLeu..... 466
856 TTTTGGTGGCAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATCA 905
467LeuProThr.....ArgAlaA 472
906 GATCTGGT...ATTGCCCTGGATGATGGATGTTTCCACTGGGTGATCAA 952
472 rgLeuGlyLysGluProAlaAspCysAspGluAspGluLeuGlyGluIle 488
953 GTATATTCAGAAATTCCTCAGCCCTCTTTTATCAACTCTCAATAT... 1000
489 LeuLysGluGluLeuProGlyProThrThrPheAspIleTyrGluPheHi 505
1000 1000
505 sPheSerAspLeuGluCysThrGluLeuAspLeuValLysCysGlyIleG 522
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522 InMetTyrTyrGluLeuGlyValValArgLysPheGlnIleProGlnGlu 538
1019 ATCATAAAATGAAAAATGCTACTCAGCTCACTAAGAAAGAAAGATGAT 1068
539 ValLeu...ValArgPheLeuPheSerIleSerLysGlyTyrArgArgII 554
1069 TACAATCAGGGTTCAGTCCACCAG...AATTTTGCTGACTTCACATTTTG 1115
554 eThrTyrHisAsnTrpArgHisGlyPheAsnValAlaGlnThrMetPheT 571
1116 CA.....ACTGGCAAAATATTGGACACATGCTCAATTAAGGGA 1156
571 hrLeuLeuMetThrGlyLysLeuLysSerTyrTyrThrAspLeuGluAla 587
1157CACATAGAT.....TC 1167
588 PheAlaMetValThrAlaGlyLeuCysHisAspIleAspHisArgGlyTh 604
1168 AAATCGAGCTATTGATCTTACGACAAAGCTTCATTAGCA..... 1207
604 rAsnAsnLeuTyrGlnMetLysSerGlnAsnProLeuAspLeuHisG 621
1208TTCATTACAAAGCATTTAGGACTTCATAAAGATTTTGATCAG 1249
621 LysSerSerIleLeuGluArgHis.....HisLeuGluPheGlyLys 634
1250 TGGGACTGCTGATTGAAGGAGATGATGAGAATCTTATTCACGGGACCAA 1299
635 Phe.....LeuLeuSerGluGluThrLeuAsnIleTyrGlnAsnLeuAs 649
1300 CATTAACACACCAATCAACACATCATG 1327
649 n...ArgArgGlnHisGluHisValIle 657

us-09-922-067-9.rsp

Mon Mar 11 10:02:21 2002

33 rgProSerValMetPheHisLysLeuGlnSerValMetSerAlaAlaGly 49
188 TTTGGCCAAACTAAAAATCCCCCGGGGAATAAGGGCTTATTTCGGTGGTG 237
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50 SerGlyHisSerLysIleProLysGlyAsnGlySerTyrrProValIglyC 66
238 TACAGACTTAATGTCTTTGATCACACTAATAAAGGGCACCTCTTGCCTTTAT 287
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66 sThrAspLeuMetPheGlyTyrrGlyAsnGluSerValPheValArgLeuT 83
288 ATTATCCATCCCAAGAATAATGATCGCTTGACACCCTTTGGATCCCAAAT 337
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83 yrTyrrProAlaGlnAspGlnGlyArgLeuAspThrValTrpIleproAsn 99
338 AAAGAATAATTTTTGGGTCTTAGCAAAATTCCTTGGACACACTGGCTTAT 387
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100 LysGluTyrrPheLeuGlyLeuSerIlePheLeuGlyThrProSerIleVa 116
388 GGGCAACAATTTTGAGGTACTCTTTGGTTCAATGACAACTCCCTCAAACT 433
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116 lGlyAsnIleLeuHisLeuLeuTyrrGlySerLeuThrThrProLasert 133
438 GGAATTCCTCCCTCTGAGGCCCTGGTGAANAATATCCACTGTGTGTTTTCT 487
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133 rPasnSerProLeuArgThrGlyGluLysTyrrProLeuIleValPheSer 149
488 CATGTCCTTTGGGCATTCAGGACACTTTATTCTGCTATTTCGCATTGACCT 537
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150 HisGlyLeuGlyAlaPheargThrIleTyrrSerAlaIleGlyIleGlyLe 166
538 GGCAATCATGGTTTATAGTTGCTGCTCTAGAACACAGAGATAGATCTG 587
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
166 uAlaserAsnGlyPheIleValIalaThrValGluHuHisArgaspArgSera 183
588 CATCTGCAACTTACTATTTCAGGCCCAATCTGCTGCAGAAAATAGGGGAC 637
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
183 laSerAlaThrTyrrPhePheGluAspGlnValAlaLaLysValGluasn 199
638 AAGTCCTTGGCTCTACCTTAGAACCTTGAACAGAGAGGAGGACACATAT 687
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200 ArgserTrpLeuTyrrLeuArgLysValLysGlnGluGluSerGluSera 216
688 ACAGAAATGACAGCTACGGCAAGAGCAAAAGAAATCTTCCCAAGCTCTCA 737
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
216 lArgLysGluGlnValGlnGlnArgAlaIleGluCysSerArgAlaLeus 233
738 GTCTGATTCCTGACATTGATCATGGAAGCCAGTGAAGAATGCATTAGAT 787
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233 erAlaIleLeuAspIleGluHisGlyAspProLysGluAsnValLeuGly 249
788 TTAAAGTTTCATATGGAACAACTGAAGGACTCTATTGATAGGCAAAAT 837
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250 SerAlaPheaspMetLysGlnLeuLysaspAlaIleaspGluThrLysIl 266
838 AGCAGTAATTTGGACATTCCTTTTGGTGGAGCAACGGTTATTCAGACTCTTA 887
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
266 eAlaLeuMetGlyHisSerPheGlyGlyAlaThrValLeuGlnAlaLeus 283
888 GTCAAGATCAGAGATTACATGCTGGTATTCGCTGGATGCATGGATGTTT 937
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938 CCACCTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCCTCTTTTAT 987
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300 ProValAsnGluGluLeuTyrrSerArgThrLeuGlnProLeuLeuPheIl 316
988 CAACCTCGAATATTTCCAATATCTCGTAAATATCATATAAAATGAAAAAT 1037
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
316 eaSnSerAlaLysPheGlnThrProLysAspIleAlaLysMetLysLysP 333
1038 GCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGG 1078
333 hetyrrinproasplysgluarglysMetIlethrIleLys 346

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DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   W03G9.6 PROTEIN.
GN   W03G9.6.
OC   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=94150718; PubMed=7906398;
RA   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA   Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA   Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA   Jones A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA   James M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA   Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA   Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkhen R.,
RA   Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA   Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT   "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT   elegans.";
RL   Nature 368:32-38(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RC   Dante M., Keppler D.;
RN   Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RC   Waterston R.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF039716; AAB96738.1;
DR   InterPro; IPR000379; Est_lip_thioest_actsite.
SQ   SEQUENCE 384 AA; 42888 MW;  FDCFLF97C162657C  CRC64;

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alignment_block:
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14 LysMetPro.....GlyGlnPheLysValGlyCysMetAspLeuMe 27
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
250 GTTTCATCAC...ACTAATAAGGCACCTCTTCGGTTTATATTATTCAT 296
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
27 tiledGluAlaIaIaGlySerGlyLeuPheMetArgLeuPhePhePro 44
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
297 CCCAAGAATAATGATCGCCTTGAC.....ACCTTTGGATCCCA 334
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
44 hr...AspSerGluIleThrGlyProSerSerLeuProValTrpIlePro 59
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
335 AATAAGAATAATTTTGGGCTTCACCAATTTCTTGA...ACACACTG 381
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
60 ArgProGlyTAlaIaIaGlyValGlyGlyLeuGlyHisSerProHi 76
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168 uGluProTyrValValGlnTyrArg.....GluIleSerAsp. 181
639 AGTCTTGCTCTACCTTAGAACCTGAAACAAGAGGAGGAGACACATATA 688
182 .....PheTyrAlaAspAlaThrValValLeu 190
689 CGAATGACAGCTAGCGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAG 738
191 GlnAsnGluArgLeuLeuPheArgGlnGlnGluIleGlnLeuLeuG 207
739 TCTGATCTTGACATT...GATCATGGAAGCCAGCTGAAGAA 778
207 nMetIleArgAsnIleAsnLeuGlyThrProAspGluAsnLeuProp 224
779 .....GCATTAGATTAAAGTTT.....GATATGGAAACAAC 811
224 heLeuCysSerValAspSerSerPheTyrAsnSerValPheGlnSerMet 240
812 AAGGACTCTATTGNT.....AGGAAAAAATAGCAGTAATGGACATTC 855
241 LysGlyAsnLeuAsnThrAlaGlnGlyGluLeuIleValAlaGlyHisSe 257
856 TTTTGGTGGAGCAACGGTT.....ATTCAGACTC 884
257 rPheGlyAlaAlaThrCysAlaPheIleSerGlySerSerThrLysSerL 274
885 TTAGTGAAGAT.....CAGAGATTTCAGATGTGGTATTGCCCTG 922
274 euTyrAsnAspTyrMetPheHisThrGluPheLysCysSerIleLeuTyr 290
923 GATGATGATGATTTCCACTGGGTGATGAAGTATATTCAGAAATTCCTCA 972
291 AspIleTrpMetLeuProValArgGlnLeuHisLeuSerThrMetArgTy 307
973 GCCC...CTCTTTTATCACTCTCAATATTTCCAATATCTCGCTAATA 1019
307 rProThrLeuMetIleIleSerTyrGluPheArgArgPheValAspAsn 324
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1107 TCACCTTTGCAACTGGCAAAATAATTTGGACACATGCTCAAAATTAAGGGA 1156
374 euProIleLeuLeuProArgMetValLeuArgValLeuLysGlyLysPhe 390
1157 GACATAGATTCAATGACGCTATTGATCTTACCACAAAGCTTCATTAGC 1206
391 GluAlaAspProTyrGluAlaLeuArgIleAsnThrArgSerSerValG 407
1207 ATTCCTTCAAAAGCATTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACT 1256
407 nPheLeuArgGluAsn.....HisValGlu..... 415
1257 GCTTGATTGAAGGAGATGATGAG.....AATCTTATT 1288
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AC O9KEX2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BH0727 PROTEIN.
GN BH0727.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
PL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001509; BAB04446.1; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
KW Complete proteome.
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Align seg 1/1 to: O9KEX2 from: 1 to: 450

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253 T.....GATCACACTAATAAGGCA 272
128 pValAspProAspArgGluGluValGluGlyValAsnGlyAsnArgGluL 145
273 CTTCTTGGTTTATATTATCCATCCCAA...GATAATGATCGCCTTGAC 319
145 euMetValArgIleTrpTyrProAlaGluLeuThrGluGlyGlyLeuLys 161
320 ACCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAGCAAAATTTCT 369
162 AlaProTyrAlaPheAspProSerTyrThrGluLeuValSerLysGluLe 178
370 TGGACACACACTGGCTTATGGGCAACATTTTGAGTTACTCTTTGGTTCAA 419
178 uProTyrTyrTyr.....LysAlaLeuLeuTyrSerValI 190
420 TGACAACTCCCTGCAAC.....TGGAAATCCCTCTGAGGCCT...GGT 460
190 leGlnThrGluThrHisSerPheAlaAsnValProValAlaAspHisGly 206
461 GAAAAATATCCACTTGTGTTTTTTCTCATGCTTGGGCGCATTCAGGAC 510
207 AlaProTyrProValLeuLeuLeuSerProGlyTyrGlyAsnSerAsnPh 223
511 ACTTTATTTCTCTATTGGCATTTGACCTGGCATCTCATGGGTTTATAGTTG 560
223 eMetTyrThrSerGlnAlaGluThrLeuAlaSerHisGlyTyrIleValC 240
561 CTGCTGTAGAACACAGAGATAGATCTGCATCTGCCAACTTACTATTTCAG 610
240 ysSerIleGluHis.....ThrTyrTyr..... 247

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252 rLeu.....PheProAspGlyArgIleValTyrGluGlnIle..... 264
711 GAGCAAAAGATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTCATCAT 760
265 .....AspLeuGluAsp 268
761 GGAAGCCAGTGAAGAATGCATTA.....GATTAAAGTT 795
269 GlyArgAspLeuAspGluGlnIleThrValTrpValAspValGlnPh 285
796 TGATATGGAACAACATGAG..... 814
285 eValLeuAspGlnLeuGlnLysTrpAsnGluSerAspProGlnAsnLeuL 302
815 .....GACTCTATTGATAGGGAATAAGCAGTAATTCGACATTCCTTT 859
302 euAsnGlyArgLeuAspMetAspArgValGlyMetLeuGlyHisSerPhe 318
860 GGTGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAGATTCAGATC 909
319 GlyGlyAlaThrAlaGlnValMetHisGlnAspProArgIleArgAl 335
910 TGGTATGCCCTGGATGATGATGATGATGATGATGATGATGATGATGAT 959
335 aclyValAsnMetAspGlyPheLeuPhe.....GlySerLeuIleCluG 350
960 CCAGAAATTCCTCAGCCCTCTTTTATCAACTCT..... 994
350 luGlyLeuAspTyrProPheMetTyrMetSerGlyValGluGluValSer 366
995 .....GAATATTTCCAAATATCCTGCTAA 1017
367 MetGluGlyProAspGlyLysValGluGluAlaGluLeuProGlu... 382
1018 TATCATAAATGAAAAATGCTACTCTACCTGATAAAGAAAG..... 1063
383 .....GluPheArgGluPheIleAlaAspLysArgLysGluG 397
1064 .....ATGATTACAATCAGGGGTTTCAGTCCAC 1090
397 lyAlaLeuLysAsnGlyLeuTyrValIleGluAsnAlaGluHis 413
1091 CAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTCGACACAT 1140
414 GluSerPheSerAspTyrMetLeuTyrSerProLeuLeuLeuAspArgAs 430
1141 GGTCAAAATTAAGGAGACATAGATTCAAATGACGATTCATTCATGCA 1190
430 pLeuProMet.....LeuAspGlnIleA 438
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seq_name: sp_bacteria:Q9F2X9

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OX NCBI_TaxID=1902;
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RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
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RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapalite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL MBL, Microbiol. 21:77-96(1996).
DR EMBL; AL392149; CAC08324.1; -.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
SQ SEQUENCE 386 AA; 40518 MW; 5F50A6B4C5D92203 CRC64;

alignment_scores:
  Quality: 206.50      Length: 289
  Ratio: 1.350        Gaps: 9
Percent Similarity: 52.941 Percent Identity: 23.875

alignment_block:
US-09-922-067-9 x Q9F2X9 ..

Align seg 1/1 to: Q9F2X9 from: 1 to: 386

290 TATCCATCCCAAGATAATGATGCGCTTGACACCCCTTTGGATGCCAAATAA 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 TyrProAlaArgSerSerGlyAlaArgProAlaAlaTyrMetThrArgSe 97

340 AGAATATTTTGGGGCTTACGACAAATTTCTTGGACACACTGGCTTATGG 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 rGlu.....AlaGlnArgLeuLeuGluLeuLysGlyLeuAlaG 110

390 GCAACATTTTGGCTTACTCTTGGTCAATGACAACTCCTCGCAACTGG 439
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
110 lyValValProAlaAlaThrValAlaGlyThrArgThrHisAlaGlnAla 126

440 AATCCCTCTGAGGCGCTGTGAAATAATCCACTGTGTGTTTCTTCTCA 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 AspAlaProAlaProGly...ArgPheProLeuValLeuLeuSerPr 142

490 TGGTCTTGGGCGATTCAGGACACTTTATCTGCTATTGGCATTCGACCTGG 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 oGlyPheSerValProArgThrThrLeuThrAlaLeuAlaValAspValA 159

540 CATCTCATGGTGTATAGTTGCTGTAGAACACAGAGATAGATCTCGCA 589
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
159 laAlaArgGlyTyrValValAlaAlaValAspHisAlaTyrGluSer... 174

590 TCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGACAA 639
174 ..... 174

640 GTCTTGGCTCTACCTTAGAACCCCTGAACACAGAGGAGGACACATATAC 689
175 .....ValG 176

690 GAAATGACAGGTAGCGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGT 739
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 lyThrGluPheProGlyGlyArgValProCysValAlaCysAspArg 192

740 CTGATTCCTTGACATTGATCATGGAAAGCCAGTGAAG...AATGCATTAGA 786

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seq_documentation_block:

ID Q9F2X9 PRELIMINARY; PRT: 386 AA.

AC Q9F2X9;

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE PUTATIVE LIPASE.

GN SC019.23C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;


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352 erpGlyGlySerThrThrGlyAlaValCysMetValAspArgArgCys 368
905 AGATGCGTATTCCCTGGATGCGATGTTTCACCTGGGTGAAGT 954
:||||:|||||:||||:   :||||:
369 AlaAlaAlaValAsnLeuAspGlyGlyAspPheAla...ProPh 384
955 ATATTCCAGAAATCTCTCAGCCCTCTTTTATCAACTCTGAATATTC 1004
||| :||| |||||:||||:   :||||:
384 eAspSerAspPheProAlaProLeuLeuMetLeuHisAlaAspLeu... 399
1005 AATATCTGCTATATCATATAAATGAAAAATGCTACTCACCTGATAA 1054
:||||:||||:   :||||:
400 .....GlyAsnPheTyrArgLeuPheGlyIleGluProProAlaArg 413
1055 GAAAGAAGATG..... 1066
||||:
414 ProArgSerPheAsnAspPheSerTyrGluArgPheGluHisAlaGlyCl 430
1067 .....ATTACAATCAGGGTTCAGTCCACACAGAAAT 1097
:||||:|||||:||||:   :||||:
430 nArgGlnAspIleHisArgLeuValLeuArgAspSerAlaHisAlaGlyL 447
1098 TTGCTGACTTCACTTTTGGCAACTGGCAAAATTAATGGACATGCTCAA 1147
:||||:||||:   :||||:
447 euthrAsp.....AsnProLeuPheIleArgArgProLeuArg 459
1148 .....TTAAGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAA 1191
||| |||||:||||:   :||||:
460 AspGlyLeuLeuGlySerAlaProThrGluValLeuIleGlnAlaProAs 476
1192 CAAGCTTCATTAGCATCTTTACAAAAGCATTTA...GCATTCATTAAG 1238
| |||||:||||:   :||||:
476 nAlaLeuValLeuGlyPhePheAspHisTyrLeuArgGlyArgAlaAsnA 493
1239 ATTTTGATCAG 1249
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493 spPheProGln 496

seq_name: sp_bacteria:Q92360

seq_documentation_block:
ID Q92360 PRELIMINARY; PRT; 391 AA.
AC Q92360;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE LIPASE.
GN SCE8.12C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=M145;
RA Chong P.P.;
RT "Molecular genetic studies on the biosynthesis and regulation of
calcium-dependent antibiotic (CDA) production by Streptomyces
coelicolor A3(2).";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035654; CAB38590.1; -.
DR EMBL; AF124138; AAD18047.1; -.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SQ SEQUENCE 391 AA; 41487 MW; E085D9332FB507CD CRC64;

alignment_scores:
Quality: 149.00 Length: 380
Ratio: 0.801 Gaps: 12
Percent Similarity: 48.947 Percent Identity: 20.000

alignment_block:
US-09-922-067-9 x Q92360 ..

Align seg 1/1 to: Q92360 from: 1 to: 391

176 GCTGCTGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCCTTA 225
||| |||||:||||:   :||||:
44 AlaAspAlaAlaTrrThrAlaSerAlaValProAlaProThrGlyAlaLe 60
226 TTCGCTGGTGTACAGACTTAATGTTTGTATCACACTAAT..... 265
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60 uProValGlyValArgThrAlaHisLeuArgAspThrSerArgArgAsp 77
266 .....AAGGGCACCTTCTTGCCTTTATATATATCA 295
77 roTrpAsnProAspArgTyrArgGluLeuAlaLeuSerLeuTrpTyrPro 93
296 TCCCAAGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATA 345
:||||:   :||||:
94 AlaLeuProSerArgAlaProArgAlaSerTyrValThrAlaArgGlu.. 109
346 TTTTGGGGTCTTAGCAAAATTTCTTGGACACACACTGGCTTATGGCC... 391
||| |||||   ||| :|||
110 .....SerAlaLeuIleLeuArgPheHisArgValGluGlyValP 123
392 .....AACATTTTGGGTTACTCTTGGTTCAATGACAACTCCTGCA 433
:||||:   :||||:
123 roAlaAspLeuLeuAlaArgPheArgValHisAlaArgThrAlaPro... 138
434 AACTGGAATTCCTCTCTG...AGGCCTGGTGAAAAATATATCCACTTGTGT 480
|||||   |||||   |||||   |||||
139 .....ProProLeuProAlaProAlaArgGlyLeuProLeuValle 152
481 TTTTCTCATGCTCTGGGCGATTCAGGACACTTTATCTGCTATTGCGCA 530
:||||:   :||||:   :||||:
152 uLeuSerProGlyPheAlaLeuProArgSerSerLeuThrGlyLeuAlaG 169
531 TTGACCTGGCATCTCATGGGTTTATAGTTCTGCTAGAACACAGAGAT 580
:|||||   :|||||   :|||||   :|||||
169 luGluLeuAlaSerArgGlyTyrAlaValAlaValAspHisAlaTyr 185
581 AGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAAT 630
:||||:   :||||:
186 GluAlaProAlaIleSerHis..... 192
631 AGGGGACAGAGTCTTGCTCTACCTTAGAACCCCTGAAACACAGAGGAGA 680
193 .....ProaspG 195
681 CACATATACGAATGACAGAGTACGGCAAGACAAAGAAATGTTCCCAA 730
:||||:   :||||:
195 lyArgValThrGlyCysLeuAlaCysArgArgHisProGluGlyAlaArg 211

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731 GCTCTCAGTCTGNTCTTCTGACATTGATCATGGAAAGCCAGTGAAGAATGC 780
212 ValAlaAla.....:|||||
781 ATTAGATTTAAAGTTTGATGATGAACAACTGAAGGACTCT.....:ThrArgAl 217
217 aalaaspleuargphevalarggluargleuLeuArgSerProGlyAlav 234
821 .....ATTGATAGGGAANAATAAGCAGTAATTTGGACATTTCT 856
234 aicglyLeuProArgLeuAspProSerArgValAlaValGlyHisSer 250
857 TTTGGTGGAGCAACGTTATTACACTCTTAGTGAAGATCAGAGATTCAG 906
251 MetGlyGlyAlaAlaAlaAlaAlaAlaLeuArgThrAspAlaGlyPheAl 267
907 ATGTGTGTTATTCCTGCTGATGATGATGTTTCCACTGGGATGATCAATAT 956
267 aalaAlaAlaAsnLeuAspGlyThrValHisThrGlyGly.....A 281
957 ATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCT...GAATATTTTC 1003
281 tgSerProValAspArgProPheLeuLeuGlyAlaGlyHisGly 297
1004 CAATATCTCTGCTAAATATCATATAAATGAAANAATGCTACTCAGCTGATAA 1053
298 ArgProGlyAlaAspProThrTrpGlnArgAlaTrpArgAspLeuSergl 314
1054 AGAAAGAAAGATGATTACAAATCAGGGGTTTCAGTCCACCAAGATTTGCTG 1103
314 yProArgArgTrpLeuSerValargGlyAlaGlyHisLeuSerPheThrA 331
1104 ACTTCAGCTTTTGCACATGCGCAAAATAATTTGCACACATGCTCAAAATAAAG 1153
331 spTyr.....:AlaArgLeuLeuGluArgThr 339
1154 GGAGACATAGATTCAATGACACTATTGAT.....CT 1185
340 GlyThrAlaGlyGluGluValThrLeuGlyAlaAlaAspAlaGlyArgVa 356
1186 TAGCAACAAGCTTCATTAGCATTTCTTACAAAAGCATTTA 1225
356 lThArggluLeuValAlaPheLeuAspGluArgLeu 369

seq_name: sp_bacteria:Q9PHC9

seq_documentation block:
ID Q9PHC9 PRELIMINARY; PRT: 795 AA.
AC Q9PHC9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DIPEPTIDYL-PEPTIDASE.
GN XF0015.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

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RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marck M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vicorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003856; AAF82828.1; -.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR Pfam; PF00326; Peptidase_S9; 1.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 795 AA; 91075 MW; ECEID9F3D51C5777 CRC64;

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alignment_scores:

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Quality: 148.50 Length: 327
Ratio: 1.046 Gaps: 16
Percent Similarity: 43.425 Percent Identity: 21.101

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alignment_block:

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US-09-922-067-9 x Q9PHC9 ..

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Align seq 1/1 to: Q9PHC9 from: 1 to: 795

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359 AGCAAAATTTCTTGGAAACACACTGGCTTATGGCAACACATTTTGAGGTTA... 406
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528 SerThrPheLysAlaLysGlnTrpIleGlnProGluTyrValGlnIlePr 544
407 .....CTCTTTGGTTCAATGACAACTCCTGCAA 434
||| ||| :|: :|: ||| ||| :|: :|: ||| |||
544 oSerLysHisGlyAlaGlyValIleTrpGlyLysTyrTyrGlyProAlas 561
435 ACTGGAATCCCTCTGAGGCTGGTGAATAATATCCACTGTGTTT 484
:|: ||| ||| :|: :|: ||| ||| :|: :|: ||| |||
561 er.....LeuGlnProGluLysArgTyrProIleValMetPhe 573
485 TCTCATGTCCTTGGGCATTCAGGACACTTTATTCCTGCTATTGCAATGA 534
||| ||| ||| :|: :|: ||| ||| :|: :|: ||| |||
574 ValHisGlyAlaGlyTyrLeuGlnAsnVal..... 583
535 CTGTCATCTCATGGGTTTATAGTTGCTGTAGAACACAGATAGAT 584
584 .....S 584
585 CTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGG 634
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
584 erAlaArgTyrProSerTyrPheArgGluGln..... 594
635 GACAAGTCTTGGCTCTACCTTAGAACCCCTGAACAAGAGAGGAGGAGACACA 684
:|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
595 .....MetPheHisThrLeuLeuValGlnLysGly..... 604
685 TATACGAAATGAGCAGGTACGCGCAAGAGCAAAAGAAATGTTCCCAAGCTC 734
604 ..... 604
735 TCAGTCTGATTTTTCACATTGAT.....CATGGAAG 766
:|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
605 ..TyrIleValLeuAspLeuAspTyrArgAlaSerAlaGlyHisGlyArg 620

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767 CCAGTGAAGAAATGATTAAGATTGATGGAACAACTGAAGCA 816
FT SIGNAL 1 48
FT CHAIN 49 310 LIPASE.
FT ACT_SITE 179 179 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 310 AA; 32649 MW; EB85B10EA649AD86 CRC64;

alignment_scores:
Quality: 120.50 Length: 373
Ratio: 0.825 Gaps: 12
Percent Similarity: 39.142 Percent Identity: 16.622

alignment_block:
US-09-922-067-9 x Q56008 ..
Align seg 1/1 to: Q56008 from: 1 to: 310

203 ATCCCGGGGAAATGGCCCTTATTCGGTGGTGTATCA.....GA 243
64 ILeGluAlaSerArgGlyProTyrAlaThrSerGlnThrSerValSerSe 80
244 CTTAAGTGTGATCACACATAAAGGCACCTCTTGGCTTTATATATC 293
80 rLeuValAlaSerGlyPheGlyGlyThr.....IleTyrTyrP 94
294 CATCCCAAGATATATGATCGCTTGCACACCTTTGGATCCCAATAAGAA 343
94 roThrSerThrAlaAsp..... 99
344 TATTTTGGGCTCTTACAAATTTCTGGAAACACACTGGCTTATGGGCA 393
100GlyThr..... 101
394 CATTTGAGGTACTCTTGGTTCATGACAACTCTGCAAACTGGAATT 443
102PheGlyAla..... 104
444 CCCCTCTGAGGCTGTGAAATAATATCCACTTGTGTTTCTCATGTT 493
105ValValIleSerProGly 110
494 CTGGGGGCAATTCAGACACTTTTCTGCTATTGGCATTTGACCTGGCATC 543
111 PheThrAlaTyrGlnSerSerIleAlaTrpLeuGlyProArgLeuAlaSe 127
544 TCATGGGTTTATAGTGTCTGTAGAACACAGAGATAGATCTGCATCTG 593
127 rGlnGlyPheValValPheThrIleAspThrAsn..... 138
594 CAACCTTACTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCT 643
138 138
644 TGGCTCTACCTTAAACCCCTGAAACAGAGAGAGAGACACATATACGAA 693
139ThrThrLeuAspGlnProAsp..... 145
694 TGACGAGTACGCGCAAGAGCAAGAAAGATGTTCCCAAGCTCTCAGCTGA 743
145 145
744 TTCTTGACATTGATCATGGAAGCCAGTGAAGAATGCATTAGATTAAAG 793
146SerArgGlyArgGlnLeuLeuSerAlaLeuAspTyrLeu 158
794 TTTGATATGGAACAACTGAAGACTCTATTGATAGGGGAAAAAATAGCACT 843
159 ThrGlnArgSerSerValArgThrArgValAlaThrArgLeuGlyVa 175
844 AATTCGACATCTTTTGGTGGAGCAACGTTTATTCAGACTCTTACTAGGAG 893
175 lMetGlyHisSerMetGlyGlyGlySerLeuGluAlaAlaLysSerA 192

seq_name: ep_bacteria:Q56008

seq_documentation_block:

ID Q56008 PRELIMINARY; PRT; 310 AA.

AC Q56008;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE LIPASE PRECURSOR (EC 3.1.1.3) (TRIACYLGLYCEROL LIPASE).

GN LIP.

OS Streptomyces SP.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1931;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 49-58.

RX MEDLINE=93138418; PubMed=8422993;

RA Perez C., Juarez K., Garcia-Castells E., Soberon G.,

RA Servin-Gonzalez L.,

RT "Cloning, characterization, and expression in Streptomyces lividans 66

RL of an extracellular lipase-encoding gene from Streptomyces sp. M11.,"

CC Gene 123:109-114(1993).

CC -1- CATALYTIC ACTIVITY: TRIACYLGLYCEROL + H(2)O = DIACYLGLYCEROL + A

CC FATTY ACID ANION.

CC -1- SUBCELLULAR LOCATION: SECRETED.

DR EMBL; M86351; AB51445.1; .

DR InterPro; IPR000379; Est_lip_thioest_actsite.

DR InterPro; IPR000734; Lipase.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.

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894 ATCAGAGATTTCAGATGGTGGTATGCTCCCTGGATGCATGGATCTTCCACTG 943
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192 rgThrSerLeuLysAlaAlaIleProLeuThrGlyTrpAsn..... 205
944 GTGTGATGAAGTATATCCAGAAATTCCTCAGCCCTCTTTTATCAACTC 993
      ||| :::::::::: :::::::::: ||| ::::::::::
206 ThrAspLysThrTrpProGluLeuArgThrProThrLeuValValGlyAl 222
994 TGAA.....TATT 1001
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222 aaSpGlyAspThrValAlaProValAlaThrHisSerLysProPheTyrg 239
1002 TCCAATATCTCTGTAATATATCAATAAATAAGAAATGAAATCTACTCCTGAT 1051
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239 luserLeuProGlySerLeu..... 245
1052 AAAGAAGAAGATGATTACAATCAGGGGTTCAGTCCAC.....CAGAA 1095
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246 ...AspLysAlaTyrlLeuGluLeuArgGlyAlaSerHisPheThrProAs 261
1096 TTTTGCTGACTTCACHTTTGCAACTGGCAAAATAAATTGGACACATGTCTA 1145
      | ::::||| ||| ::::|||
261 nThrSerAspThrThrIleAla..... 268
1146 AATTAAAGGAGACATAGATTCAATGCAGCTATTGATCTTACCAACAAA 1195
      ::::
269 ..... 269
1196 GCTTCATTAGCAATCTTCAAAAGCAATTTAGGACTTCATAAAGATTTTGA 1245
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270 TyrSerIleSerTrpLeuLysArgPheIleAspSerAspThrArgTyrgI 286
1246 TCAGTGGGACTGCTTGATT 1264
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286 uGlnPheLeuLysProIle 292
seq_name: sp_bacteria:p73946
seq_documentation_block:
ID P73946 PRELIMINARY; PRT; 622 AA.
AC P73946;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHEtical 68.8 KDA PROTEIN.
GN SLR1506.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima T., Hirose M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90911; BAA18013.1;
DR InterPro; IPR000379; Est.Lip.thioest_actsite.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 622 AA; 68847 MW; B41028F5EA6BDA1A CRC64;

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alignment_scores:

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Quality: 119.00 Length: 351
Ratio: 0.708 Gaps: 16
Percent Similarity: 47.863 Percent Identity: 21.368

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alignment_block:

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US-09-922-067-9 x P73946 ..
Align seq 1/1 to: P73946 from: 1 to: 622

385 TATGGGCAACATTTTGAGGTTACTCTTTGGTTCAATGACAACATCTCTGCAA 434
      ||||| :::: ||| ::::::::::||| :::: ||| ::::
257 TyrGlyValAlaProLysGluThrTrpTrpLeuAsnAspGlnSerArgAs 273
435 ACTGGAAATTC.....CCCTCTCGAGGCGCTGGTGA... 463
      : ::::|||
273 nArgArgPheTyrlValAspValTyrlArgProGln..ArgTrpLysGluGly 289
464 AAATATCCACTGTGTGTTTTTCTCATGGTCTTGGGGCATTCAGGACACT 513
      ||| ::::::::::||| ||| ::::
290 LysThrProValLeuValPheSerHisGlyLeuAlaSerArgProGluAs 306
514 TTATTTCTGCTATTTGGCATTCACCTGGCATCTCATGGGTTTATAGTTGCTG 563
      :::: ||| ::::::::::||| :::: ||| ::::
306 pPheAspAsnAlaAlaGluLysMetAlaSerTyrlGlyPheValValAla 323
564 CTGTGAACAC.....AGAGAT 580
      : ::::|||
323 euProGlnHisProGlySerAspIleLeuGlnAlaGlnAlaLeuLeuAsn 339
581 AGATCTGCATCTGCAACTTACTATTCTTCAAGGACCAATCTGTCGCAAAAT 630
      ||| :::: ||| ::::
340 ArgThrSerArgGlnGlyTyrlTyrl.....ProThrGluPh 351
631 AGGGGACAAGTCTTGCTCTACCTTAGAACCTGAACACAGAGAGAGGAGA 680
      : |||
351 eIleAsp.....ArgProLysAspIleS 359
681 CACATATACGAAATGACAGGTACGGCAAGCAAGCAAAAGAAATGTCCCAA 730
      ::::||| :::: ||| :::: ||| ::::
359 erTyrlValIleAspGluLeuGluArgArgAsnAlaSerGluPheGlyAsp 375
731 GCTCTAGTCTGATCTTGTGATTCATGTAAGGAGCCAGTGAAGAATGC 780
      ||| :::: |||
376 ArgLeuAsnLeu..... 379
781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTATAGGG 830
380 .....T 380
831 AAAAAATAGCAGTAATTTGACATTTTGGTGAGCAACGGTTATTTCAG 880
      ::::||| ||| :::: ||| :::: ||| ::::
380 hrGlnValGlyValGlyGlyHisSerPheGlyGlyTyrlGlyAlaLeuAla 396
881 ACTCTTAGTGAAGATCAGAGATTCAGATGTTGCTGCTGCTGCTGCTGCTG 930
      :::: ||| :::: ||| :::: |||
397 Val.....AlaGlyAlaThrIleAsp...Tr 404
931 GATGTTTTCACCTGGGTGAT...GAAGTATATTCAGAAATTCCTCAGCCCC 977
      : ||| :::: ||| :::: ||| :::: ||| ::::
404 pAspPheLeuLysSerGluCysArgIleGlyGlnGlyValProAsnThrA 421
978 TCTTTTATCAACTCTGATATTTCCAAATATCTGCTAATATCATATAAA 1027
      :::: ||| :::: ||| ::::
421 laLeuLeuLeuGlnCysAspAlaLeuThrLeuProArgSerAspTyrlAsp 437
1028 ATGAANAATGCTACTCACCCTGATAAAGAAAGAAAGATGATTAATCAATCAG 1077
      : :::: ||| :::: ||| :::: ||| ::::
438 Phe.....ArgAspProArgValValAlaAlaVal 447
1078 GGGTTCAGTCCACCAGAAATTTGCTGACTTC...ACTTTTGCACTGGCA 1124
      :::: ||| ||| ||| :::: |||
447 uAlaAlaAsnProValAsnSerAlaIlePheGlyValSerGlyLeuHisL 464
1125 AAATAATTGGACATGCTCAATTAAGGAGACATAGATTCAAATGCA 1174
      ||::: :::: ||| ||| :::: |||
464 yValThrValProValLeuLeuLeuGlySerTyrlAspProAlaThr 480
1175 GCTATTGATCTTAGCAACAAAGCTTCA.....TTAGCATCTTACA 1215

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481 ProPheValLeuGluGlnAlaArgSerPheProArgLeuAlaSerArgAs 497
1216 AAAGCATTTAGGACTT.....CATAAGATTTTTCATCAGT 1250
497 pLysTyrLeuThrLeuMetGluGlnAlaHisValAspPheSerLysI 514
1251 GGCACGTCTTGATGAAGGAGATGAGAGTCTT..... 1285
514 LeAspAlaAsnIleLysAsnValGluSerValGluAlaValSerLeu 530
1286 ...ATTCCAGGGACCAAC...ATTACACACCAATCAACACATGTT 1329
531 LysLeuProAsnProAsnLeuHisThrTyrGlySerAlaValMetVa 547
1330 A 1330
547 I 547

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seq_name: sp_bacteria.Q59798

seq_documentation_block:

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ID Q59798 PRELIMINARY; PRT; 304 AA.
AC Q59798;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE LIPASE PRECURSOR (EC 3.1.1.3) (TRIACYLGLYCEROL LIPASE).
GN LIP.
OS Streptomyces albus g.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299159; PubMed=8026751;
RA Cruz H., Perez C., Wellington E., Castro C., Servin-Gonzalez L.;
RT "Sequence of the Streptomyces albus G lipase-encoding gene reveals the
RT presence of a prokaryotic lipase family."
RL Gene 144:141-142(1994).
CC -1- CATALYTIC ACTIVITY: TRIACYLGLYCEROL + H(2)O -> DIACYLGLYCEROL + A
CC FATTY ACID ANION.
CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
DR EMBL; U03114; AA53485.1; -
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 42 POTENTIAL.
FT CHAIN 43 304 LIPASE.
FT ACT_SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 304 AA; 31984 MW; F2CA16ABD1AF2AB2 CRC64;

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alignment_scores:
  Quality: 117.50 Length: 371
  Ratio: 0.778 Gaps: 11
  Percent Similarity: 40.701 Percent Identity: 17.790

alignment_block:
US-09-922-067-9 x Q59798 ..
Align seg 1/1 to: Q59798 from: 1 to: 304

194 CAACATAAATCCCGGGGAATGGCTTATCCGTTGGTGTGACA... 241
55 ArgAlaSerIleGluAlaProArgGlyProTyrAlaValSerGlnThrSe 71
242 .....GACTTAATGTTGATCACACTAATAGGCGACCTTCTCGGTT 284
71 rValSerSerLeuValValSerGlyPheGlyGlyThr.....I 85
285 TATATATCCATCCCAAGATAATGATCGCTTGACACCCCTTTGGATCCCA 334

```

```

85 leTyrTyrProThrSerThrGlyAsp..... 93
335 AATAAAGAATAATTTTGGGGCTTAGCAAAATTTCTTGAACACACTGGCT 384
94 .....GlyThr..... 95
385 TATGGGCAACATTTTGGAGTTACTCTTTGGTTCAATGACAACCTCCTGCAA 434
96 .....PheGlyAla..... 98
435 ACTGGAATTCCTCTGAGGCTGTGTGAAAAATATCCACTTGTGTTT 484
99 .....ValValVal 101
485 TCTCATGCTCTTGGGGCATTTCCAGACACTTTTATTCTGCTATTGGCATTGA 534
102 ThrProGlyPheThrAlaThrGluSerSerMetAlaThrLeuGlyProAr 118
535 CTGGCATCTCATGGGTTTATAGTTGCTGCTGTAGAACACACAGATAGAT 584
118 gLeuAlaSerGlnGlyPheValValPheThrIleAsp..... 130
585 CTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGG 634
130 ..... 130
635 GACAAGCTTGGCTCTACCTTAGAACCTTGAACAAAGAGGAGGAGACACA 684
131 .....ThrLeuThrThrLeuAspGlnProAsp..... 139
685 TATACGAATGACAGGTACGGCAAGCAAGCAAAAGAAATGTTCCCAAGCTC 734
139 ..... 139
735 TCAGTCTGATCTTGTGACATTGATCATGGAAGCCAGTGAAGATGCATTA 784
140 .....SerArgGlyArgGlnMetLeuAlaLeu 149
785 GATTTAAAGTTTATGTAACCAACTGAAGGACTCTATTGATAGGGAATA 834
150 AspTyrLeuThrGluArgSerSerAlaArgThrArgIleAspGlyThrAr 166
835 AATAGCAGTAATGGACATCTTTTGGTGGAGCAACGGTTATTCAGACTC 884
166 gLeuGlyValIleGlyHisSerMetGlyGlyGlyThrLeuGluAla 183
885 TTAGTGAAGATCAGAGATTCAGATGCTGTTATGCCCTGGATGATGATG 934
183 lalYssSerArgProSerLeuLysAlaAlaIleProLeuThrProTrpAsn 199
935 TTTCCACTGGTGCATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTT 984
200 Leu.....AspLysThrTrpProGluValThrThrProThrLeuVa 213
985 TATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAATGAAA 1034
213 lValGlyAlaAspGlyAspThrValAlaProValAlaThrHisAlaLys 230
1035 AATGCTACTACCTGATAAAGAAAGAGATGATTACAATCAGGGGTCA 1084
230 roPheTyrSer.....SerLeuProSerSer 238
1085 GTCACACAGAATTTTGTGCTTACCTTCACTTTTGAACCTGGCAAAATATGG 1134
239 ThrAspArgAlaTyrLeuGluLeuAsnAlaThr..... 250
1135 ACATATGCTCAAAATTAAGGAGACATAGATTCAAATGCAGCTATTGATC 1184
251 .....HisPheAlaProAsnL 256
1185 TTAGCAAC.....AAGCTTCATTAGCATCTTACAAAGCAT 1222

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550 GTTTATAGTTGCTGCTGTAGAACACAGAGATAGATGTCATCTGCAACTT 599
|
109 Y..... 109
600 ACTATTTCAGGACCAATCTCTGCAGAAATAGGGGACAGCTTTGGCTC 649
: : : : : ||| : : |||||
110GluserGluGlySerLysThrIleGlyAsp..... 120
650 TACCTTTAGAACCCCTGAACAAGAGGAGGAGACACATATACGAAATGACGA 699
120 120
700 GGTACGGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATCTTGT 749
120 120
750 ACATTGATCATGAAAGCCAGTGAAGAAATGCATTAGATTAAAGTTTCAT 799
121lysGluIleuAspLeuSerGlyAla 129
800 ATGGAAACAACACTGAAGGACTCTATTGTATAGGAAAAAATAGCAGTAATTGG 849
: : : : : ||| : : : : : |||||
130 IleAspTrpLeuLeuSerAsnThrLysLysIleAlaLeuIleGI 146
850 ACATTCTTTTGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGA 899
| : : : : : ||| : : : : : |||||
146 yPheSerMetGlyAlaMetValThrIleArgAlaLeuAlaGluAspGluA 163
900 GATTACAGATGTGGTATTTGCCCTGATGCATGGATGTTTCCACTGGGTGAT 949
|| : : : : : ||||| : : : : : |||
163 rgValCysCysGlyIleAlaAspSerProIleTyrIle.....Asp 177
950 GAAGTATATCCAGAAATTCCTCAGCCCTCTTTTTCATCAACTCTGAATA 999
: : : : : : : : : : : : : : : |||
178 LysThrGlyAlaArgGlyLeuLys.....TyrPheAlaAsnLeuProGI 192
1000 TTTCCAATATCTGCTTAATATCATATAAA...ATGAAAAAATGCCTACTCAC 1046
||| ||||| : : : : : |||
192 uPheLeuTyrPro.....IleIleLysProPheThrLysMetPheSerG 207
1047 CTGATAAGAAAGAAAGATGATTACAACTAGGGGTTCCAGTCCACACG 1093
||| ||||| : : : : : |||
207 lyAlaLysGluAlaAsnIleIleAspTyrAlaAspLysValArgLys 222

```

178 LysThrGlyAlaArgGlyLeuIys.....TyrPheAlaAsnLeuProGI 192
      :::::
      :::::
      :::::
1000 TTTCCAATATCTGCTAAATATCATATAAA...ATGAAAAAATGCTACTAC 1046
      ||| ||||| |||||
192 uPheLeuTyrPro.....IleIleIysProPheThrIysMetPheSerG 207
      :::::
      :::::
      :::::
1047 CTGATAAAGAAGAAGATGATTACAATCAGGGGTTGAGTCCACGAC 1093
      ||||| :::::
      :::::
207 lyAlaIysGluValAsnIleIleAspTyrAlaAspLysValArgIys 222
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      :::::
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seq_documentation_block:
ID Q47900 PRELIMINARY; PRT: 711 AA.
AC Q47900;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DIPEPTIDYL PEPTIDASE IV.
OS Flavobacterium meningosepticum.
OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae;
OC Chryseobacterium.
NCBI_TaxID=238;
[1]
SEQUENCE FROM N.A.
MEDLINE=95314307; PubMed=7793970;
KABashima T., Yoshida T., Ito K., Yoshimoto T.;
*Cloning, sequencing, and expression of the dipeptidyl pepti-
gene from Flavobacterium meningosepticum in Escherichia coli
Arch. Biochem. Biophys. 320:123-128(1995).
EMBL: D42121; BAA07702.1; -.
MEROPS: S09.013; -.
InterPro: IPR002469; DPPIV_N term.
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR InterPro: IPR001375; Peptidase_S9.
DR InterPro: IPR002471; Prol_endopep_ser.
DR Pfam: PF00930; DPPIV_N term; 1.
DR Pfam: PF00326; Peptidase_S9; 1.

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RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.
 RL DNA Res. 5:55-76(1998).
 DR EMBL; AP000002; BAA29683.1; ..
 DR InterPro; IPR000379; Est_lip_thioest_actsite.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 622 AA; 73231 MW; 6D4BABA1A2614E02 CRC64;

alignment_scores:
 Quality: 110.00 Length: 290
 Ratio: 0.932 Gaps: 14
 Percent Similarity: 40.690 Percent Identity: 20.345

alignment_block:

US-09-922-067-9 x 058323 ..

Align seg 1/1 to: 058323 from: 1 to: 622

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344 TATTTTGGGGT.....CTTAGCAAAATTTCTTGGACACA 378
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287 TyrLeuTrpAspGlyGluValArgGluIleAlaLys.....GlyLysHI 301
|||||.....|
379 CTGGCTTATGGGC.....AACATTTTGAGTTTACTCTTTGGTT 416
|||||.....|
301 strpileMetGlyPheAspAlaAspGluArgLeuIleTyrLeuLysGluT 318
|||||.....|
417 CAATGACAACTCTCCAAAC.....TGGAATTCC..... 445
:: ||| |||||:: |||||::
318 hrAlaThrArgProAlaGluLeuTyrLeuTrpAspGlyGluGluArgGln 334
||| ||| |||||:: |||||::
445 .....TyrSerGluAsp..... 445
335 LeuThrAspTyrAsnGlyLeuIlePheLysLysLeuLysThrPheGluPr 351
445 ..... 445
351 oArgHisPheArgPheLysSerIleAspLeuGluLeuAspGlyTrpTyrI 368
446 .....CCTCTAGGCGCTGGTGAATAATCCACTTTGTTGTTTCT 487
||||| ||||| ||||| ||||| ||||| |||||
368 leLysProGluIleLysGluGlyGluLysAlaProValIleValPheVal 384
488 CATGGT.....CTTGGGGCATTCAGGACACTTTATCTGCTATTGGCAT 531
||||| ||| :: ||| ::
385 HisGlyGlyProLysGlyMetTyrGlyTyrPheLysTyrGluMetGI 401
532 TGACCTGGCATCTCATGGTGTATAGTCTGCTGTAGAACACAGAGATA 581
||||| ||||| ||||| ||||| |||||
401 nLeuMetAlaSerLysGlyTyrTyrIleValTyrValAsnProArgGlyS 418
582 GATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATA 631
||||| ||| ||| |||||
418 eAsnGly.....TyrSerGluAsp..... 424
632 GGGGACAAAGTCTGGCTCTACCTTAGAACCTTGAACACAGAGAGAGAC 681
||||| ||||| ||||| ||||| |||||
425 .....PheAlaLeuArgValLeu.....GluArgTh 433
682 ACATATACGAAATGAGCAGGTAGCGCAAGCAAGCAAGCAAGCAAGTCT 731
||||| ||| |||
433 rGlyLeuGluAspPheGln..... 439
732 CTCTCACTCTGATCTTGTGACATTCATGTAAGCAAGCCAGTGAAGTGA 781
||||| ||||| |||||
440 .....AspIleLeuAsnGly 444
782 TTAGATTAAAGTTTATATGACACAACTGAGGACTCTATTGATAGGA 831
||||| ||||| ||||| ||||| |||||
445 IleGlu.....GluPheLeuArgLeuGluProGlnAlaAspArgGI 458
832 AAAAATAGCAGTAATTTGGATTTCTTTTGGTGGAGCAACGGTATTTCAGA 881
||||| ||||| ||||| ||||| |||||
458 uArgIleGlyIleThrGlyIleSerTyrGlyTyrMetThrAsnTrpA 475

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882 CTCTTAGTGAAGATCAGAGATTCAGATCTGCTGTTATGGC..... 919
|||||.....|
475 laLeuThrGlnSerAspLeuPheLysAlaGlyIleSerGluAsnGlyIle 491
920 .....CTGGATGCATGATGTTT..... 937
||||| ||||| |||||
492 SerTyrTrpLeuThrSerTyrAlaPheSerAspIleGlyLeuTrpPheAs 508
938 .....CCACTGGGTGATGAGTATATATTCAGAA 965
||||| ||||| |||||
508 pLysGluValIleGlyAspAsnProLeuGluAsnGluAsnTyrArgLysL 525
966 TTCTCTCAGCCCTCTTTT 985
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525 eu....SerProLeuPheTyr 530
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seq_documentation_block:
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AC 087543;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN ADHESIN (FRAGMENT).
OS Capnocytophaga gingivalis.
OC Bacteria; CF8 group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DR2001;
RA Tempco P.J.;
RT "Capnocytophaga outer-membrane adhesin DNA sequence, 3'end.";
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083393; AAC35353.1; -.
DR MROPS; S09.013; -.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR001375; Peptidase_S9.
DR InterPro; IPR002471; Prol_endopep_ser.
DR Pfam; PF00326; Peptidase_S9; 1.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
FT NON_TER
SO SEQUENCE 237 AA; 27482 MW; 4D630AC81D64EDAC CRC64;

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alignment_scores:

Quality: 108.50 Length: 240
 Ratio: 0.986 Gaps: 9

Percent Similarity: 45.833 Percent Identity: 20.833

alignment_block:

US-09-922-067-9 x 087543 ..

Align seg 1/1 to: 087543 from: 1 to: 237

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419 ATGACAACCTCTGCAAACTGGAATTCCTCTCAGGCCCTGGTGAATAA 468
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15 MetIleLysProSerAspPheAsnGlu.....AsnLysLys 27
469 TCCACTTCTTGTGTTTCTTCAT...GGTCTGGGCATTCAGACACTTT 515
||||| ||||| ||||| ||||| |||||
27 rProLeuLeuMetPheGlnTyrSerGlyProGlySerGlnValHisA 44
516 ATTCGTCTATTGGCATTCAC.....CTGGCATCTCAT 547
||||| ||||| |||||
44 snSerPheSerGlyPheAspThrPheTrpTyrMetLeuAlaGlnLys 60
548 GGGTTTATAGTCTGCTGCTAGACACACAGATAGATCTGCATCTCAAC 597
||||| ||||| ||||| ||||| |||||
61 GlyTyrIleValLeuLysValAspGlyArgGlyThrGlyTyrLysGlyAl 77
598 TTACTATTTCAGGACCAATCTGCTCCAGAAATAGGGACAACTCTTGGC 647

```

```

77 aaalaPhe.....LysLysCyst 83
648 TCTACCTTAGAACCCCTGAACAAGAGGAGGACACACATATACGAATGAG 697
83 hrTyrLysGlnLeuGlyLysTyrGluLeuGluAspGlnValGluAla 99
698 CAGGTACGGCAAGAGCAAGAAAGATGTTCCCAAGCTCTCAGTCTGATTCT 747
100 LysIleValGlyAsnTyrLys..... 106
748 TGACATTGATCATGGAAGCCAGTCAGAAATGCATTAGATTAAAGTTTG 797
106 ..... 106
798 ATATGGAACAACCTGAAGNCTCTATTGATAGGGAAGAAATAGCAGTAATT 847
107 .....TyrIleAspLysAspArgIleGlyIleTyr 116
848 GGACATTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCA 897
117 GlyTyrSerPheGlyGlyPheMetAlaSerAsnCysIleLeuArgGlyG 133
898 GAGATTTCAGATGTGTATTGCC.....CTGGATGCATGGATGTTT. 937
133 uMetPheLysMetSerIleAlaValAlaProValThrAsnTyrArgPheT 150
938 .....CCACTGGGTGATGAAGTATATCCAGAAATTCCTCAG.....CCC 976
150 yrAspThrValTyrThrGluArgTyrMetGlnThrProGlnGluAsnPro 166
977 CTCCTTTTATCAACTCTCAATATTTCCAAATATCTCTGCTAAATATCATAA 1026
167 GluGlyTyrAspAsnAsnSerProLeuThrTyrAlaLysAsnLeu..... 181
1027 AATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACATCA 1076
182 .....AsnLysLysPheLeuLeuValH 189
1077 GGGGTTCACTCCACCAGAAAT 1096
189 isGlyThrAlaAspAsn 195
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 seconds
(without alignments)
4.528 Million cell updates/sec

Title: us-09-922-067-10
Sequence: 1 QYINPVA 7

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_1101.*

1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	10	AA01944	N-terminus #1 of p
2	37	100.0	441	AA01944	Human acetyl hydro
3	37	100.0	441	AA01944	Human acetyl hydro
4	37	100.0	441	AA01944	Human acetyl hydro
5	37	100.0	441	AA01944	Human acetyl hydro
6	37	100.0	441	AA01944	Human acetyl hydro
7	37	100.0	441	AA01944	Human acetyl hydro
8	37	100.0	441	AA01944	Human acetyl hydro
9	37	100.0	441	AA01944	Human acetyl hydro
10	37	100.0	441	AA01944	Human acetyl hydro
11	37	100.0	441	AA01944	Human acetyl hydro

12	37	100.0	441	16	AA01944	Human acetyl hydro
13	37	100.0	441	16	AA01944	Human plasma plate
14	37	100.0	441	18	AA01944	Human platelet-act
15	37	100.0	441	18	AA01944	Human plasma plate
16	37	100.0	441	18	AA01944	Platelet-activatin
17	37	100.0	441	19	AA01944	Human plasma plate
18	37	100.0	441	20	AA01944	Human plasma plate
19	37	100.0	441	20	AA01944	Human PAF-AH prote
20	37	100.0	441	21	AA01944	Plasma platelet-ac
21	37	100.0	441	21	AA01944	Human low density
22	37	100.0	441	21	AA01944	Human platelet-act
23	37	100.0	441	21	AA01944	Human PAF-AH prote
24	37	100.0	441	22	AA01944	Human plasma plate
25	37	100.0	441	22	AA01944	Human plasma plate
26	37	100.0	441	22	AA01944	Human plasma plate
27	37	100.0	441	22	AA01944	Human plasma plate
28	37	100.0	441	22	AA01944	Human plasma plate
29	37	100.0	441	22	AA01944	Human plasma plate
30	37	100.0	441	22	AA01944	Human plasma plate
31	37	100.0	441	22	AA01944	Human plasma plate
32	37	100.0	441	22	AA01944	Human platelet-act
33	37	100.0	441	22	AA01944	Human platelet-act
34	37	100.0	441	22	AA01944	Human plasma plate
35	37	100.0	441	22	AA01944	Human plasma plate
36	37	100.0	441	22	AA01944	Human plasma plate
37	37	100.0	441	22	AA01944	Human plasma plate
38	37	100.0	441	22	AA01944	Platelet-activatin
39	37	100.0	441	22	AA01944	Human T-cell lymph
40	37	100.0	441	22	AA01944	Corn diacylglycerol
41	32	86.5	155	21	AA01944	Corn diacylglycerol
42	32	86.5	285	21	AA01944	Corn diacylglycerol
43	32	86.5	327	21	AA01944	Corn diacylglycerol
44	32	86.5	361	21	AA01944	Corn diacylglycerol
45	32	86.5	500	21	AA01944	Rice diacylglycerol

ALIGNMENTS

RESULT 1

AA01944
ID: AA01944 standard; peptide; 10 AA.

AC AA01944;

DT 18-SEP-2000 (first entry)

DE N-terminus #1 of purified recombinant human LDL-PLA2.

XX Human; low density lipoprotein associated phospholipase A2;
XX LDL-PLA2; plasma PAF acetyl hydroxylase; recombinant; purification;
XX short chain phospholipid; serine-dependant phospholipase;
XX inflammation; proinflammatory; anti inflammatory; drug screening;
XX antibody; diagnosis; N-terminus.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..10

FT /note= "Corresponds to residues 22-31 of full-length
human LDL-PLA2 (AA01944)"

XX WO200024910-A1.

XX 04-MAY-2000.

XX 27-OCT-1999; 99WO-GB03551.

XX 28-OCT-1998; 98GB-0023647.

XX 28-OCT-1998; 98GB-0023648.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX

PI Boyd H, Tew DG;
 DR WPI; 2000-350749/30.
 XX

PT Recombinant low density lipoprotein associated phospholipase A2, used
 PT to produce antibodies for diagnostics, is purified using a Blue
 PT Sepharose and Q Sepharose column -
 XX

PS Examples; Page 13; 28pp; English.
 XX

CC The invention relates to a method for purifying recombinant low density
 CC lipoprotein-associated phospholipase A2 (LDL-PLA2). The method comprises
 CC applying a cell extract, supernatant or solution containing the
 CC recombinantly expressed LDL-PLA2 to a zinc chelating column, applying
 CC the eluate to a Blue Sepharose column, and applying that eluate to a Q
 CC Sepharose column. The invention also provides a process which
 CC additionally comprises the prior steps of constructing a vector
 CC comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment
 CC thereof, expressing the tagged protein in a host cell, isolating the
 CC tagged protein from the harvest medium or cell lysate, purifying the
 CC protein using a metal matrix affinity column (preferably a nickel
 CC column), and removing the histidine tag by protease cleavage. LDL-PLA2,
 CC also known as plasma PAF acetyl hydroxylase, is a serine-dependent
 CC phospholipase which catalyses the hydrolysis of phospholipids with short
 CC chain acyl groups at the sn-2 position. Its in vivo role is not known -
 CC due to its ability to hydrolyse both phospholipids with short chain sn-2
 CC substituents (which often arise from oxidative cleavage of longer chain
 CC sn-2 substituents) and PAF, it may be either a pro-inflammatory enzyme or
 CC an anti-inflammatory enzyme, depending on the precise in vivo role
 CC adopted. LDL-PLA2 can be used in structural and mechanistic studies to
 CC elucidate the activity of the enzyme in vivo. The enzyme may be used to
 CC screen and identify compounds which modulate its activity, and to raise
 CC antibodies for use in diagnostics. Sequences AAB01944-B01946 represent
 CC three different N-terminal sequences obtained from purified recombinant
 CC human LDL-PLA2.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 37; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYINPVA 7
 DB 4 qyinpva 10
 |||||

RESULT 2

AAR73048
 ID AAR73048 standard; Protein; 441 AA.

AC AAR73048;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C291S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX

OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 291
 FT /note= "Wild-type Cys is substd. by Ser."

PN W09509921-A.

PD 13-APR-1995.

PF 06-OCT-1994; 94WO-US11340.

XX

PR 06-OCT-1993; 93US-0133803.
 XX (ICOS-) ICOS CORP.
 XX

PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX

DR WPI; 1995-155262/20.
 XX

XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX

PS Example 10; ; 88pp; English.
 XX

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX

SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYINPVA 7
 DB 25 qyinpva 31
 |||||

RESULT 3

AAR73049
 ID AAR73049 standard; Protein; 441 AA.

AC AAR73049;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C334S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX

OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 334
 FT /note= "Wild-type Cys is substd. by Ser."

PN W09509921-A.

PD 13-APR-1995.

PF 06-OCT-1994; 94WO-US11340.

PR 06-OCT-1993; 93US-0133803.
 XX

PA (ICOS-) ICOS CORP.
 XX

PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX

DR WPI; 1995-155262/20.
 XX

PT New nucleic acid encoding platelet activating factor,
 XX

PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 PS Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 DB 25 qyinpva 31
 |||||

RESULT 4

AAR73050
 ID AAR73050 standard; Protein; 441 AA.

AC AAR73050;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C407S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 407

FT /note- "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original

CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

DB 25 qyinpva 31
 |||||

RESULT 5

AAR71920

ID AAR71920 standard; Protein; 441 AA.

AC AAR71920;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant S108A.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 108

FT /note- "Wild-type Ser is substd. by Ala."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

XX The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match

100.0%; Score 37; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
|||||||
Db 25 qyinpva 31

RESULT 6

AAR71921
ID AAR71921 standard; Protein; 441 AA.

XX AC AAR71921;

XX XX 06-DEC-1995 (first entry)

XX XX Human acetyl hydrolase (AH) mutant S273A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 273 /note= "Wild-type Ser is substd. by Ala."

XX PN WO9509921-A.

XX XX 13-APR-1995.

XX XX 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,
XX PT acetyl-hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; : 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match

Best Local Similarity 100.0%; Score 37; DB 16; Length 441;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
|||||||
Db 25 qyinpva 31

RESULT 7

AAR71922

ID AAR71922 standard; Protein; 441 AA.

XX AC AAR71922;

XX DT 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D296A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 296 /note= "Wild-type Asp is substd. by Ala."

XX PN WO9509921-A.

XX PD 13-APR-1995.

XX XX 06-OCT-1994; 94WO-US11340.

XX PR 06-OCT-1993; 93US-0133803.

XX PA (ICOS-) ICOS CORP.

XX XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;

XX DR WPI; 1995-155262/20.

XX PT New nucleic acid encoding platelet activating factor,
XX PT acetyl-hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy

XX PS Example 10; : 88pp; English.

XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).

XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.

XX SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
|||||||
Db 25 qyinpva 31

RESULT 8

AAR71923

ID AAR71923 standard; Protein; 441 AA.

XX AC AAR71923;

XX XX 06-DEC-1995 (first entry)

XX DE Human acetyl hydrolase (AH) mutant D338A.

XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX KW disease; pleurisy; diagnosis.

```
XX OS Homo sapiens.
XX PF
XX PR Key Location/Qualifiers
XX FT Misc-difference 338
XX FT /note= "Wild-type Asp is substd. by Ala."
XX PN
XX XX
XX PD
XX PD 13-APR-1995.
XX PF 06-OCT-1994; 94WO-US11340.
XX PR 06-OCT-1993; 93US-0133803.
XX XX (ICOS-) ICOS CORP.
XX XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX XX WPI; 1995-155262/20.
XX DR
XX XX New nucleic acid encoding platelet activating factor,
XX FT acetyl:hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX XX
XX PS Example 10; ; 88pp; English.
XX XX
XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 qyinpva 31

RESULT 10
AAR71925
ID AAR71925 standard; Protein; 441 AA.
XX XX
XX AC AAR71925;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE
XX DE Human acetyl hydrolase (AH) mutant H395A/H399A.
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; Inflammatory;
XX KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 395
XX FT /note= "Wild-type His is substd. by Ala."
XX FT 399
XX FT /note= "Wild-type His is substd. by Ala."
XX XX
XX PN W09509921-A.
XX XX
XX PD 13-APR-1995.
XX XX
XX PF 06-OCT-1994; 94WO-US11340.
XX PR 06-OCT-1993; 93US-0133803.
XX XX (ICOS-) ICOS CORP.
XX XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX XX WPI; 1995-155262/20.
XX DR
XX XX New nucleic acid encoding platelet activating factor,
XX FT acetyl:hydrolase - useful in diagnosis and for treating
XX PT inflammatory diseases, e.g. pleurisy
XX XX
XX PS Example 10; ; 88pp; English.
XX XX
XX CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
XX CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
XX CC made with single amino acid changes for the purposes of identifying
XX CC the active site of AH. The sequences of these mutants are not given
XX CC in the patent specification; they have been derived from the original
XX CC wild-type protein (AAR71913).
XX CC The AH gene and its product are useful in the treatment of inflammatory
XX CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
XX CC gene may also be used in raising monoclonal antibodies specific for AH
XX CC that are useful in the diagnosis of such diseases.
XX SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 qyinpva 31

RESULT 9
AAR71924
ID AAR71924 standard; Protein; 441 AA.
XX XX
XX AC AAR71924;
XX XX
XX DT 06-DEC-1995 (first entry)
XX DE
XX DE Human acetyl hydrolase (AH) mutant H351A.
XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; Inflammatory;
XX KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 351
XX FT /note= "Wild-type His is substd. by Ala."
XX XX
XX PN W09509921-A.
XX XX
XX PD 13-APR-1995.
```

PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Example 10; : 88pp; English.
 XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 |||||
 Db 25 qyinpva 31

RESULT 11
 AAR73046
 ID AAR73046 standard; Protein; 441 AA.
 XX
 AC AAR73046;
 XX
 XX 06-DEC-1995 (first entry)
 XX
 XX Human acetyl hydrolase (AH) mutant C675.
 XX
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 67 /note- "Wild-type Cys is substd. by Ser."
 FT
 XX W09509921-A.
 XX
 XX 13-APR-1995.
 XX
 XX 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 XX
 XX (ICOS-) ICOS CORP.
 XX
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Example 10; : 88pp; English.

CC The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.
 XX
 XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 |||||
 Db 25 qyinpva 31

RESULT 12
 AAR73047
 ID AAR73047 standard; Protein; 441 AA.
 XX
 AC AAR73047;
 XX
 XX 06-DEC-1995 (first entry)
 XX
 XX Human acetyl hydrolase (AH) mutant C229S.
 XX
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 229 /note- "Wild-type Cys is substd. by Ser."
 FT
 XX W09509921-A.
 XX
 XX 13-APR-1995.
 XX
 XX 06-OCT-1994; 94WO-US11340.
 XX
 XX 06-OCT-1993; 93US-0133803.
 XX
 XX (ICOS-) ICOS CORP.
 XX
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 XX Example 10; : 88pp; English.
 XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX
SQ Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 qyinpva 31
|||||

RESULT 13

AA71913
ID AAR71913 standard; Protein; 441 AA.

XX
AC

XX AC

DT 05-DEC-1995 (first entry)

XX

DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX WO9509921-A.

PN 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX N-PSDB; AAQ87947.

XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Claim 5; Page 53-54; 88pp; English.

XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX purified. The platelet activating factor acetyl hydrolase (AAR71913)
XX is useful in the treatment of inflammatory diseases, in particular
XX pleurisy, asthma, rhinitis and eczema. The gene may also be used in
XX raising monoclonal antibodies specific for PAF-AH that are useful in
XX the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 qyinpva 31
|||||

RESULT 14

AAW26498
ID AAW26498 standard; Protein; 441 AA.

XX

AC AAW26498;

XX 05-JAN-1998 (first entry)

XX Human platelet-activating factor acetylhydrolase.

XX Platelet-activating factor acetylhydrolase; PAF-AH; human;
KW inflammation; asthma; pleurisy; necrotising enterocolitis;
KW adult respiratory distress syndrome; therapy.

XX Homo sapiens.

XX US5656431-A.

XX 12-AUG-1997.

XX 06-OCT-1993; 93US-0133803.

XX 07-JUN-1995; 95US-0483232.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;
PI Wilder CL;

XX WPI; 1997-414580/38.

XX N-PSDB; AAT87048.

XX Detecting lesions in human platelet-activating factor
PT acetylhydrolase gene - by comparison with defined wild-type gene
PT sequence

XX Example 3; Column 47-50; 53pp; English.

XX This polypeptide comprises human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH), a protein that inactivates PAF and
XX inactivates oxidatively fragmented phospholipids such as products of
XX the arachidonic acid cascade that mediate inflammation. Its
XX sequence was deduced from a full-length cDNA clone (see AAT87048)
XX obtained from a macrophage cDNA library. Mouse, dog, cattle,
XX chicken, rat and macaque PAF-AH polypeptides (see AAW26500-505) have
XX also been identified. Recombinant PAF-AH polypeptides can be
XX produced in prokaryotic or eukaryotic host cells and used to mimic
XX or augment normal processes of resolution of inflammation in vivo.
XX Examples describe the in vivo therapeutic effect of recombinant
XX PAF-AH products on acute inflammation, pleurisy, asthma,
XX necrotising enterocolitis and adult respiratory distress syndrome
XX in animal models.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 18; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 qyinpva 31
|||||

RESULT 15

AAW23796
ID AAW23796 standard; Protein; 441 AA.

XX AAW23796;

XX 04-NOV-1997 (first entry)

XX Human plasma platelet activating factor acetylhydrolase.

KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
 KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
 KW central nervous system shock; arthritis; Crohn's disease;
 KW systemic lupus erythematosus; adult respiratory distress syndrome.

XX Homo sapiens.

XX US5641669-A.

XX 24-JUN-1997.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Tjoelker LW, Trong HL;

PI Wilder CL;

XX WPI; 1997-340947/31.

XX N-PSDB; AAT80564.

PT New human plasma platelet activating factor acetylhydrolase -
 PT useful as anti-inflammatory for treatment of asthma, anaphylaxis,
 PT shock, etc

XX Claim 1; Column 35-38; 43pp; English.

XX The present sequence represents the purified and isolated human plasma
 CC platelet activating factor acetylhydrolase (PAF-AH). This novel
 CC polypeptide inactivates PAF and oxidatively fragmented phospholipids
 CC such as pro-inflammatory arachidonic acid metabolites, and so can be
 CC used to treat inflammation by augmenting endogenous activity. Typical
 CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
 CC central nervous system shock, arthritis, Crohn's disease, systemic
 CC lupus erythematosus, adult respiratory distress syndrome. The
 CC polypeptide can also be used to raise specific antibodies (Ab) which
 CC are useful as immunoassay reagents and for generating anti-idiotypic
 CC antibodies. The nucleic acid encoding the protein can be used to screen
 CC for related genes; in hybridisation assays to assess the protein-
 CC producing cells; to generate knockout mice; to detect genetic mutations
 CC and (antisense sequences) to inhibit the protein expression. Unlike PAF
 CC receptor antagonists, the protein is a natural component of plasma.

XX Sequence 441 AA;

Query Match 100.0%; Score 37; DB 18; Length 441;

Best Local Similarity 100.0%; Pred. NO. 8.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

Db 25 qyinpva 31

Search completed: March 9, 2002, 00:31:57

Job time: 443 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:33:00 ; Search time 47.03 Seconds
(Without alignments)
3.349 Million cell updates/sec

Title: US-09-922-067-10

Perfect score: 37

Sequence: 1 QYINPVA 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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3: /cgn2_6/ptodata/2/1aa/5A-COMB.pep.*

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5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	7	2	US-08-557-892-10
2	37	100.0	7	2	US-08-387-858A-10
3	37	100.0	7	4	US-09-294-384B-10
4	37	100.0	441	1	US-08-470-187-8
5	37	100.0	441	1	US-08-318-905-8
6	37	100.0	441	1	US-08-483-232-8
7	37	100.0	441	1	US-08-483-140-8
8	37	100.0	441	2	US-08-485-938A-8
9	37	100.0	441	2	US-08-910-041-8
10	37	100.0	441	3	US-09-328-474-8
11	37	100.0	441	3	US-09-100-546-8
12	37	100.0	441	4	US-09-010-715-8
13	37	100.0	441	4	US-09-577-758-8
14	29	78.4	27	2	US-08-557-892-3
15	29	78.4	27	2	US-08-387-858A-3
16	29	78.4	27	4	US-09-294-384B-3
17	29	78.4	282	3	US-09-136-442-4
18	29	78.4	520	4	US-08-482-728A-4
19	29	78.4	520	4	US-09-028-366-5
20	28	75.7	272	1	US-08-252-995D-14
21	28	75.7	272	2	US-08-834-108-14
22	28	75.7	541	2	US-08-484-438-6
23	28	75.7	603	4	US-09-198-122-2
24	28	75.7	621	2	US-08-419-652-4
25	28	75.7	660	1	US-08-248-532-3
26	28	75.7	660	2	US-08-419-652-3
27	28	75.7	662	1	US-08-248-532-2

28	75.7	662	2	US-08-419-652-2	Sequence 2, Appli
29	75.7	662	2	US-08-685-118-4	Sequence 4, Appli
30	75.7	662	2	US-08-915-495-4	Sequence 4, Appli
31	75.7	662	2	US-08-914-520-4	Sequence 4, Appli
32	75.7	662	3	US-08-789-350-2	Sequence 2, Appli
33	75.7	705	2	US-08-456-647B-4	Sequence 4, Appli
34	75.7	705	2	US-08-237-401A-4	Sequence 4, Appli
35	75.7	718	2	US-08-974-565C-7	Sequence 7, Appli
36	75.7	718	3	US-09-255-748-7	Sequence 7, Appli
37	75.7	1308	2	US-08-484-438-2	Sequence 2, Appli
38	73.0	22	3	US-09-101-146-32	Sequence 32, Appli
39	73.0	77	4	US-09-246-500B-7	Sequence 7, Appli
40	73.0	257	3	US-09-101-146-6	Sequence 6, Appli
41	73.0	345	3	US-09-101-146-1	Sequence 1, Appli
42	73.0	477	3	US-08-843-982B-8	Sequence 8, Appli
43	73.0	478	4	US-09-272-114-1	Sequence 1, Appli
44	73.0	478	4	US-09-249-338-2	Sequence 2, Appli
45	73.0	548	2	US-09-032-315-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-557-892-10
; Sequence 10, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557.892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387.858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-557-892-10

Query Match 100.0%; Score 37; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 1 QYINPVA 7
| | | | |
DB 1 QYINPVA 7

RESULT 2

US-08-387-858A-10
; Sequence 10, Application US/08387858A
; Patent No. 5981252
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858A
; FILING DATE: 24 February 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
US-08-387-858A-10

Query Match 100.0%; Score 37; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 1 QYINPVA 7
| | | | |
DB 1 QYINPVA 7

RESULT 3

US-09-294-384B-10
; Sequence 10, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,384B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
US-09-294-384B-10

Query Match 100.0%; Score 37; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 1 QYINPVA 7
| | | | |
DB 1 QYINPVA 7

RESULT 4

US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl

us-09-922-067-10.rai

Mon Mar 11 10:01:48 2002

```

;
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-187-8

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Query Match 100.0%; Score 37; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QYINPVA 7
Db 25 QYINPVA 31

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RESULT 6
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689

```

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;
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-187-8

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Query Match 100.0%; Score 37; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QYINPVA 7
Db 25 QYINPVA 31

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RESULT 5
US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-232-8

Query Match 100.0%; Score 37; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 7
US-08-483-140-8
; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-140-8

Query Match 100.0%; Score 37; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 8
US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-938A-8

Query Match 100.0%; Score 37; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 9
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:

;; APPLICANT: Cousens, Lawrence S.
;; APPLICANT: Eberhardt, Christine D.
;; APPLICANT: Gray, Patrick W.
;; APPLICANT: Le Trong, Hai
;; APPLICANT: Tjoelker, Larry W.
;; APPLICANT: Wilder, Cheryl L.
;; TITLE OF INVENTION: Platelet-Activating Factor
;; TITLE OF INVENTION: Acetylhydrolase
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/910,041
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/483,232
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rin-Laures, Li-Hsien
;; REGISTRATION NUMBER: 33,547
;; REFERENCE/DOCKET NUMBER: 27866/34026
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-910-041-8

Query Match 100.0%; Score 37; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 10
US-08-910-041-8
; Sequence 8, Application US/09328474
; Patent No. 6043794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase

;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/328,474
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/483,232
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rin-Laures, Li-Hsien
;; REGISTRATION NUMBER: 33,547
;; REFERENCE/DOCKET NUMBER: 27866/34026
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-328-474-8

Query Match 100.0%; Score 37; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 11
US-09-100-546-8
; Sequence 8, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 100.0%; Score 37; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 12
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 100.0%; Score 37; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 13
US-09-577-758-8
Sequence 8, Application US/09577758
Patent No. 6203790
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,758
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/010,715
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6203790and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-577-758-8

Query Match 100.0%; Score 37; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 14
US-08-557-892-3
Sequence 3, Application US/08557892
Patent No. 5968818
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/557,892
FILING DATE: 14 No. 5968818ember 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,858
FILING DATE: 14 No. 5968818ember 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-557-892-3

Query Match 78.4%; Score 29; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINP 5
Db 1 QYINP 5

RESULT 15
US-08-387-858A-3
Sequence 3, Application US/08387858A
Patent No. 5981252
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/387,858A
FILING DATE: 24 February 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-387-858A-3

Query Match 78.4%; Score 29; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINP 5
Db 1 QYINP 5

Search completed: March 9, 2002, 00:33:01
JOB time: 402 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:11 ; Search time 53.53 Seconds
(without alignments)
9.961 Million cell updates/sec

Title: US-09-922-067-10

Perfect score: 37

Sequence: 1 QYINPVA 7

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: PIR_68:*
- 2: pir1:*
- 3: pir2:*
- 4: pir3:*
- 5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	100.0	441	2 S60247	platelet-activatin
2	32	86.5	231	2 T01294	sterol O-acyltrans
3	32	86.5	441	2 H84576	diacylglycerol O-a
4	32	86.5	520	2 T52584	diacylglycerol O-a
5	32	86.5	605	2 S52253	copper resistance
6	32	86.5	716	1 WZBEE6	77.8K DNA helicase
7	32	86.5	723	1 RRMOTN	RNA-directed RNA p
8	31	83.8	764	2 T39878	hypothetical prote
9	31	83.8	771	2 F70701	probable biof2 pro
10	31	83.8	1417	2 H83132	probable sensor/re
11	30	81.1	149	2 S75155	hypothetical prote
12	30	81.1	248	2 S34595	surface lipoprotei
13	30	81.1	283	2 S65961	manu protein - Par
14	30	81.1	430	2 T32426	hypothetical prote
15	30	81.1	454	2 S58148	hypothetical prote
16	30	81.1	698	2 C82332	translation elonga
17	30	81.1	753	2 S35371	finger protein neu
18	29	78.4	154	2 T14727	dehydrin DHN1 - so
19	29	78.4	235	2 T32462	hypothetical prote
20	29	78.4	295	2 B86320	3-phosphoserine ph
21	29	78.4	295	2 T51362	phosphoserine phos
22	29	78.4	333	2 S34347	GTP-binding regula
23	29	78.4	411	2 B69450	anthranilate synth
24	29	78.4	414	2 A24872	hypothetical prote
25	29	78.4	421	2 C82253	folypolylglutamate
26	29	78.4	444	2 T38760	hypothetical prote
27	29	78.4	462	2 H69751	amino acid permeas
28	29	78.4	520	1 S64705	cyclophilin-like p
29	29	78.4	524	2 T06021	hypothetical prote

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf,

W. Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:9780132; PIDN:AC50126.1; PID:9780133

Query Match 100.0%; Score 37; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7

Db 25 QYINPVA 31

RESULT 2

T01294

sterol O-acyltransferase homolog F27F23.26 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 30-Apr-1999

C:Accession: T01294

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;

submitted to the EMBL Data Library, May 1998

A:Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.

A:Reference number: Z14177

A:Accession: T01294

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-231 <ROD>

A:Cross-references: EMBL:AC003058; NID:g3135250; PID:g3135276

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 2

A:Introns: 44/3; 70/3; 104/3; 150/2; 177/3; 184/3; 205/3

A>Note: F27F23.26

Query Match 86.5%; Score 32; DB 2; Length 231;

Best Local Similarity 83.3%; Pred. No. 14;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

myb-related protei
hypothetical prote
DNA helicase/prima
genome polypotein
hypothetical prote
hypothetical prote
TATA box-binding p
alkaline phosphata
pleiotropic drug r
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
ig kappa chain . h
hypothetical 15.7K
yafM protein - Esc
hypothetical prote

Qy 1 QYINPV 6
|||||
Db 104 QYINPI 109

RESULT 3
H84576
diacylglycerol O-acyltransferase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84576
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <STO>
A:Cross-references: GB:AE002093; NID:94191775; PIDN:AA010144.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19450
A:Map position: 2

Query Match 86.5%; Score 32; DB 2; Length 441;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
|||||
Db 269 QYINPI 274

RESULT 4
T52584
diacylglycerol O-acyltransferase (EC 2.3.1.20) [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 17-Nov-2000
C:Accession: T52584
R:Hillis, M.J.; Lu, C.; Hobbs, D.H.
PNAS Lett. 452, 145-149, 1999
A:Title: Cloning of a cDNA encoding diacylglycerol acyltransferase from Arabidopsis thaliana
A:Reference number: Z26127
A:Accession: T52584
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-520 <HIL>
A:Cross-references: EMBL:AJ131831; PIDN:CAB44774.1
A:Experimental source: cultivar Columbia
C:Function:
A:Description: EC 2.3.1.20 [validated; MUID:99313150]; catalyzes the final acylation of
A:Pathway: triacylglycerol biosynthesis
C:Keywords: acyltransferase; coenzyme A

Query Match 86.5%; Score 32; DB 2; Length 520;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
|||||
Db 331 QYINPI 336

RESULT 5
S52253
copper resistance protein pcoa precursor - Escherichia coli plasmid pRJ1004
N:Alternate names: copper-binding protein
C:Species: Escherichia coli

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jun-1999
C:Accession: S70159; S52253
R:Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.
Mol. Microbiol. 17, 1153-1166, 1995
A:Title: Molecular genetics and transport analysis of the copper-resistance deter.
A:Reference number: S70159; MUID:96130847
A:Accession: S70159
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-605 <BRO>
A:Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58525.1; PID:g619128
C:Genetics:
A:Gene: pcoa
A:Genome: plasmid pRJ1004
C:Superfamily: laccase
C:Keywords: copper binding
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-605/Product: copper resistance protein pcoa #status predicted <MAT>

Query Match 86.5%; Score 32; DB 2; Length 605;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
|||||
Db 299 QYINPV 304

RESULT 6
WZBPE6
77.8K DNA helicase/primase-associated protein - equine herpesvirus 1 (strain Ab4p)
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: I36800
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: I36800
A:Molecule type: DNA
A:Residues: 1-716 <TEL>
A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802489.1; PID:g330845
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MUID:92295566
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 54
C:Superfamily: varicella-zoster virus gene 52 protein

Query Match 86.5%; Score 32; DB 1; Length 716;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPVA 7
|||||
Db 430 QHINPVA 436

RESULT 7
RWOTN
RNA-directed RNA polymerase (EC 2.7.7.48) - tobacco necrosis virus (strain A)
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: 23K protein
C:Species: tobacco necrosis virus, TNV
A:Note: host Phaseolus vulgaris (kidney bean)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999
C:Accession: A35523

R:Meulewaeter, F.; Seurinck, J.; van Emmelo, J.
 Virology 177, 699-709, 1990
 A:Title: Genome structure of tobacco necrosis virus strain A.
 A:Reference number: A35523; MUID:90320143
 A:Accession: A35523
 A:Molecule type: genomic RNA
 A:Residues: 1-723 <MEU>
 A:Cross-references: EMBL:M33002; NID:gl172549; PIDN:AAA86434.1; PID:g310915
 A:Note: readthrough of the terminator UAG occurs between codons AAA for 202-Lys and GGG
 C:Superfamily: carnation mottle virus RNA-directed RNA polymerase: barley yellow dwarf
 C:Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication
 F:1-202/Product: 23K protein #status predicted <KPP>
 F:427-593/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BYD>

Query Match 86.5%; Score 32; DB 1; Length 723;
 Best Local Similarity 71.4%; Pred. NO. 49;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 Db 419 KYVNPVA 425
 :|||:|

RESULT 8
 T39878
 hypothetical protein SPBC20F10.07 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39878
 R:Lyne, M.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
 submitted to the EMBL Data Library, February 1998
 A:Reference number: Z21888
 A:Accession: T39878
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-764 <LYN>
 A:Cross-references: EMBL:AL021747; PIDN:CAA16847.1; GSPDB:GN00067; SPDB:SPBC20F10.07
 A:Experimental source: strain 972h-; cosmid c20F10
 C:Genetics:
 A:Gene: SPDB:SPBC20F10.07
 A:Map position: 2

Query Match 83.8%; Score 31; DB 2; Length 764;
 Best Local Similarity 85.7%; Pred. NO. 87;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 Db 489 QYKPA 495
 ||| |||

RESULT 9
 F70701
 probable bioP2 protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Feb-2000
 C:Accession: F70701
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: F70701
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-771 <COL>
 A:Cross-references: GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02417.1; PID:e266944;
 A:Experimental source: strain H37RV
 C:Genetics:

A:Gene: bioF2
 C:Superfamily: glycine C-acetyltransferase homology
 C:Keywords: phosphoprotein; pyridoxal phosphate
 F:615/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 83.8%; Score 31; DB 2; Length 771;
 Best Local Similarity 83.3%; Pred. NO. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7
 Db 721 YVNPVA 726
 |:||||

RESULT 10
 H83132
 probable sensor/response regulator hybrid PA4112 [imported] - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83132
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1417 <STO>
 A:Cross-references: GB:AE004827; GB:AE004091; NID:g9950306; PIDN:AAG07499.1; GSPDB:G
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4112

Query Match 83.8%; Score 31; DB 2; Length 1417;
 Best Local Similarity 85.7%; Pred. NO. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 Db 147 QYIEPVA 153
 ||| |||

RESULT 11
 S75155
 hypothetical protein sl11638 - Synecocystis sp. (strain PCC 6803)
 C:Species: Synecocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S75155
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 S.

A:Reference number: S74322; MUID:97061201
 A:Accession: S75155
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-149 <KAN>
 A:Cross-references: EMBL:D90903; GB:AB001339; NID:gl652127; PIDN:BAAL7069.1; PID:d10
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 81.1%; Score 30; DB 2; Length 149;
 Best Local Similarity 66.7%; Pred. NO. 24;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7
 |:|:|

Db 44 YVNP1A 49

RESULT 12

S34995
surface lipoprotein p27 - Lyme disease spirochete (strain B29)
N;Alternate names: 27k antigen
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: strain B29
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S34995; S27487
R;Reindl, M.; Redl, B.; Stoeffler, G.
Mol. Microbiol. 8, 1115-1124, 1993
A;Title: Isolation and analysis of a linear plasmid-located gene of Borrelia burgdorferi
A;Reference number: S34995; MUID:93368427
A;Accession: S34995
A;Molecule type: DNA
A;Residues: 1-248 <REI>
A;Cross-references: EMBL:M85216; NID:g469167; PIDN:AAA17494.1; PID:g144008
A;Experimental source: Borrelia burgdorferi B29
C;Keywords: surface antigen

Query Match 81.1% Score 30; DB 2; Length 248;
Best Local Similarity 86.7% Pred. No. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6

||:||||
Db 197 QYLNPI 202

RESULT 13

S65961
mauN protein - Paracoccus denitrificans
C;Species: Paracoccus denitrificans
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
C;Accession: S65961
R;van der Palen, C.J.N.M.; Slotboom, D.J.; Jongejans, L.; Reijnders, W.N.M.; Harms, N.;
Eur. J. Biochem. 230, 860-871, 1995
A;Title: Mutational analysis of mau genes involved in methylamine metabolism in Paracoccus
A;Reference number: S65958; MUID:95324575
A;Accession: S65961
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <VAN>
A;Cross-references: EMBL:U15028; NID:g595839; PIDN:AAA86469.1; PID:g595843
C;Genetics:
A;Gene: mauN
A;Superfamily: hypothetical protein H10346; ferredoxin 2[4Fe-4S] homology
F;220-280/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 81.1% Score 30; DB 2; Length 283;
Best Local Similarity 57.1% Pred. No. 48;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 7

||:||||
Db 159 EYVNPVS 165

RESULT 14

T32426
hypothetical protein C10E2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T32426
R;Wohlmann, P.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C10E2.
A;Reference number: 221165
A;Accession: T32426

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-420 <WOH>

A;Cross-references: EMBL:AF026202; PIDN:AAE71242.1; GSPDB:GN00028; CESP:C10E2.2

A;Experimental source: strain Bristol N2; clone C10E2

C;Genetics:

A;Gene: CESP:C10E2.2

A;Map position: X

A;Introns: 5/2; 80/3; 160/3; 191/2; 245/2; 302/2; 335/3

C;Superfamily: Caenorhabditis elegans hypothetical protein C10E2.2

Query Match 81.1% Score 30; DB 2; Length 420;
Best Local Similarity 71.4% Pred. No. 75;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPV 7

||:||||
Db 364 QYENPVS 370

RESULT 15

S58148
hypothetical protein SPAC2F7.04 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 04-Mar-2000
C;Accession: T38352; S58148
R;Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
A;Reference number: 221799
A;Accession: T38352

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-454 <GE2>

A;Cross-references: EMBL:250142; NID:g1052783; PIDN:CAA90491.1; PID:g1052787; GSPD

A;Experimental source: strain 972h-; cosmid c2F7

C;Genetics:

A;Gene: SPAC2F7.04

A;Map position: 1

A;Introns: 78/3; 294/3

C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC2F7.04

Query Match 81.1% Score 30; DB 2; Length 454;
Best Local Similarity 85.7% Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPV 7

||:||||
Db 103 QYNNPVA 109

Search completed: March 9, 2002, 00:34:13
Job time: 324 sec

Mon Mar 11 10:01:50 2002

us-09-922-067-10.rpr

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:36 ; Search time 30.16 seconds
(without alignments)
8.510 Million cell updates/sec

Title: US-09-922-067-10
Perfect score: 37
Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	441	1 PAPA_HUMAN	Q13093 h platelet-
2	32	86.5	605	1 PCOA_ECOLI	Q47452 escherichia
3	32	86.5	716	1 HEPA_HSVB	P28946 equine herp
4	32	86.5	723	1 RRPO_TNVA	P22958 tobacco nec
5	30	81.1	283	1 MAUN_PARDE	Q51660 paracoccus
6	30	81.1	454	1 YAZA_SCHPO	Q09696 schizosacch
7	29	78.4	265	1 RUZA_DROME	Q9V498 drosophila
8	29	78.4	353	1 GEO_LYNST	P38411 lymanaea sta
9	29	78.4	411	1 TRPE_ARCFU	Q28669 archaeoglob
10	29	78.4	414	1 GAG2_DROME	P20828 drosophila
11	29	78.4	444	1 YAS2_SCHPO	Q10138 schizosacch
12	29	78.4	462	1 YBNG_BACSU	P54425 bacillus su
13	29	78.4	525	1 YBF4_YEAST	P34219 saccharomyc
14	29	78.4	791	1 TEX_BORPE	Q45388 bordetella
15	29	78.4	1407	1 T2D2_YEAST	P23255 saccharomyc
16	29	78.4	1499	1 CDR2_CANAL	P78595 candida alb
17	29	78.4	1511	1 PDR5_YEAST	P33302 saccharomyc
18	29	78.4	1529	1 PDRF_YEAST	Q04182 saccharomyc
19	29	78.4	1829	1 BIR6_HUMAN	Q9NR09 homo sapien
20	28	75.7	143	1 YDRA_RHORO	P14301 rhodospiril
21	28	75.7	165	1 YAFM_ECOLI	Q47152 escherichia
22	28	75.7	222	1 ERBA_RAT	P62956 rattus norv
23	28	75.7	287	1 NAPH_HAEIN	P44653 haemophilus
24	28	75.7	344	1 VGLM_HSV6U	Q04630 human herpe
25	28	75.7	344	1 VGLM_HSV6Z	P52449 human herpe
26	28	75.7	346	1 OPSP_ICTPU	Q42266 ictalurus p
27	28	75.7	451	1 AGAL_ECOLI	P06720 escherichia
28	28	75.7	503	1 C303_DROME	Q9V399 drosophila
29	28	75.7	503	1 NQRB_CHLMU	Q9PKB6 chlamydia m
30	28	75.7	575	1 PTL_HAEIN	P43922 haemophilus
31	28	75.7	603	1 PLK1_HUMAN	P53350 homo sapien
32	28	75.7	603	1 PLK1_MOUSE	Q07832 mus musculu
33	28	75.7	603	1 PLK1_RAT	Q62673 rattus norv

RESULT 1
PAPA_HUMAN ID PAPA_HUMAN STANDARD; PRT; 441 AA.
AC Q13093: Q15692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
GN PLA2G7 OR PAFAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.
RC TISSUE=Myeloid;
RX MEDLINE=95214779; PubMed=7700381;
RA Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,
RA Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,
RA Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;
RA "Anti-inflammatory properties of a platelet-activating factor
acetylhydrolase.";
RL Nature 374:549-553(1995).
[2]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Lymphoma;
MEDLINE=96197208; PubMed=8624782;
RX Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,
RA Moores K., Gloger I.S., Macphee C.H.;
RA "Purification, properties, sequencing, and cloning of a lipoprotein-
associated, serine-dependent phospholipase involved in the oxidative
modification of low-density lipoproteins.";
RL Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).
[3]
MUTAGENESIS.
MEDLINE=96029630; PubMed=7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
Gray P.W.;
RA "Plasma platelet-activating factor acetylhydrolase is a secreted
phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
[4]
VARIANT PRE-279.
MEDLINE=96259525; PubMed=8675689;
RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,
RA Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,
RA McIntyre T.M., Gray P.W., Prescott S.M.;
RA "Platelet-activating factor acetylhydrolase deficiency. A missense
mutation near the active site of an anti-inflammatory
phospholipase.";
RL J. Clin. Invest. 97:2784-2791(1996).
[5]

P12374 pseudomonas
Q95263 homo sapien
P42701 homo sapien
P52891 saccharomyc
P17922 bacillus su
P50401 cellulomona
P51826 homo sapien
Q15303 homo sapien
P43071 candida alb
O15015 homo sapien
O46382 bos taurus
Q9Y666 homo sapien

ALIGNMENTS

RP VARIANT PHE-279.
RX MEDLINE-98430412; PubMed-9759612;
RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
RA Yoshimizu N., Fukushi K., Satoh K.;
RT "A mutation in plasma platelet-activating factor acetylhydrolase
RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
RL for hypertension.";
Thromb. Haemost. 80:372-375(1998).
CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2O) = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
CC RESPONSES.
CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).

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DR EMBL; U20157; AAC50126.1; -;
DR EMBL; U24577; AAB04170.1; -;
DR MIM; 601690; -;
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000734; Lipase
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 441
FT ACT_SITE 273 273 PLATELET-ACTIVATING FACTOR
FT ACT_SITE 296 296 ACETYLHYDROLASE.
FT ACT_SITE 351 351 CHARGE RELAY SYSTEM.
FT CARBOHYD 423 423 CHARGE RELAY SYSTEM.
FT CARBOHYD 433 433 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
FT PROTEIN).
FT /FTID-VAR_004268.
FT MUTAGEN 108 108 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT MUTAGEN 273 273 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.
FT MUTAGEN 286 286 D->N: DIMINISHED ACTIVITY.
FT MUTAGEN 296 296 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.
FT MUTAGEN 304 304 D->A: NO CHANGE IN ACTIVITY.
FT MUTAGEN 338 338 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
FT MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.
FT CONFLICT 379 379 V -> A (IN REF. 2).
SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

Query Match 100.0%; Score 37; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QYINPVA 7
Db 25 QYINPVA 31

RESULT 2

PCOA_ECOLI
ID PCOA_ECOLI STANDARD; PRT; 505 AA.
AC Q47452; 2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COPPER RESISTANCE PROTEIN A PRECURSOR.
GN PCOA.
OS Escherichia coli.
OG Plasmid PRJ1004.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / ED8739;
RX MEDLINE-96130847; PubMed-8594334;
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T.O., Rouch D.A.;
RT "Molecular genetics and transport analysis of the copper-resistance
RT determinant (pco) from Escherichia coli plasmid pRJ1004";
RL Mol. Microbiol. 17:1153-1166(1995).
CC -1- FUNCTION: REQUIRED FOR THE COPPER-INDUCIBLE EXPRESSION OF COPPER
CC RESISTANCE. MAY HAVE OXIDASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. COPA
CC SUBFAMILY.

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DR EMBL; X83541; CAA58525.1; -;
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_Oxidase2.
DR Pfam; PF00394; Cu-oxidase; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Repeat; Signal; Plasmid; Metal-binding;
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 605 COPPER RESISTANCE PROTEIN A.
FT DOMAIN 382 429 3 X 8 AA TANDEM REPEATS OF D-H-X-X-M-X-
FT G-M.
FT REPEAT 382 389 1.
FT REPEAT 414 421 2.
FT REPEAT 422 429 3.
FT METAL 100 100 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 102 102 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 142 142 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 144 144 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 538 538 COPPER (TYPE 1) (POTENTIAL).
FT METAL 541 541 COPPER (TYPE 2) (POTENTIAL).
FT METAL 543 543 COPPER (TYPE 3) (POTENTIAL).
FT METAL 586 586 COPPER (TYPE 3) (POTENTIAL).
FT METAL 587 587 COPPER (TYPE 1) (POTENTIAL).
FT METAL 588 588 COPPER (TYPE 3) (POTENTIAL).
FT METAL 592 592 COPPER (TYPE 1) (POTENTIAL).
FT METAL 597 597 COPPER (TYPE 1) (POTENTIAL).
SQ SEQUENCE 605 AA; 67307 MW; 8EECA182D56B27D8 CRC64;

Query Match 86.5%; Score 32; DB 1; Length 605;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QYINPV 6
Db 299 QYINPV 304

CC Necrovirus.
 CC NCBI_TaxID=12055;
 CC
 RN [1]
 RN
 RP SEQUENCE FROM N.A.
 RP MEDLINE=90320143; PubMed=2371773;
 RX Meulawaeter F., Seuring J., van Emmelo J.;
 RA "Genome structure of Tobacco Necrosis virus strain A.";
 RT Virology 177:699-709(1990).
 RL
 CC -1- MISCELLANEOUS: READTHROUGH OF A TERMINATOR CODON OCCURS BETWEEN
 CC CODONS FOR LYS-202 AND GLY-203.
 CC
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 CC reasons.

Query Match 81.1%; Score 30; DB 1; Length 283;
 Best Local Similarity 57.1%; Pred. No. 30;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 II IIII
 DB 159 EYVNPVS 165

RESULT 6
 YA24_SCHPO STANDARD: PRT; 454 AA.
 ID Q09696;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE HYPOTHETICAL 51.4 KDA PROTEIN C2F7.04 IN CHROMOSOME I.
 GN SPAC2F7.04.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; 250142; CAA90491.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 454 AA; 51390 MW; C6366431E1E6758C CRC64;

Query Match 81.1%; Score 30; DB 1; Length 454;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 II IIII
 DB 103 QYINPVA 109

RESULT 7
 RUZA_DROME STANDARD: PRT; 265 AA.
 ID RUZA_DROME
 AC Q9V4Q8;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROBABLE U2 SMALL-NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').
 GN CG1406.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceolaxer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -|- FUNCTION: THIS PROTEIN IS ASSOCIATED WITH SN-RNP U2. IT HELPS THE
 CC A' PROTEIN TO BIND STEM LOOP IV OF U2 SNRNA (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -|- SIMILARITY: CONTAINS 3 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 CC EMBL; AE003840; AAF59207.1; -
 DR HSSP; P09661; IAGN.
 DR FlyBase; FBgn0033210; CG1406.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003603; LRRcap.
 DR Pfam; PF00560; LRR; 2.
 DR SMART; SM00446; LRRcap; 1.
 DR Nuclear protein; RNA-binding; Ribonucleoprotein; Leucine-rich repeat;
 KW REPEAT.
 FT REPEAT 41 63 LRR 1.
 FT REPEAT 64 87 LRR 2.
 FT REPEAT 88 111 LRR 3.
 SQ SEQUENCE 265 AA; 29744 MW; FB09D8D1D96501A5 CRC64;

Query Match 78.4%; Score 29; DB 1; Length 265;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINP 5
 II IIII
 DB 14 QYINP 18

RESULT 8
GBQ_LYMST
ID P38411; STANDARD; PRT; 353 AA.
AC
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
ON NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95324523; PubMed=7601100;
RA Knol J.C., Ramnath Singh S., van Kesteren E.R., van Minnen J.,
RA Planta R.J., van Heerikhuizen H., Vreugdenhil E.;
RT "Cloning of a molluscan G protein alpha subunit of the Gq class which
is expressed differentially in identified neurons.";
RL Eur. J. Biochem. 230:193-199(1995).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
CC -----
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CC -----
CC EMBL; Z23106; CAA80653.1; -.
DR PIR; S34347; S34347.
DR HSSP; P04896; LAZT.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00442; GPROTEINAQ.
DR GTP-binding; Transducer; Multigene family; ADP-ribosylation;
KW Palmitate; Lipoprotein.
FT LPID 3 3 PALMITATE (BY SIMILARITY).
FT LPID 4 4 PALMITATE (BY SIMILARITY).
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 199 203 GTP (BY SIMILARITY).
FT NP_BIND 268 271 GTP (BY SIMILARITY).
FT MOD_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY).
SQ SEQUENCE 353 AA; 41565 MW; 980F7604E952A3FD CRC64;

Query Match 78.4%; Score 29; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINP 5
Db 94 QYINP 98
|||||

RESULT 9
TRPE_ARCFU
ID TRPE_ARCFU STANDARD; PRT; 411 AA.
AC O28669;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.1.3.27).
GN TRPE OR AF1603.

OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
ON NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Karlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fliedmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTHRANILATE +
PYRUVATE + L-GLUTAMATE.
CC -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC -!- SUBUNIT: Tetramer of two components I and two components II (BY
SIMILARITY).
CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
FAMILY.
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CC -----
CC EMBL; AF000992; AAB89646.1; -.
DR TIGR; AF1603; -.
DR InterPro; IPR000350; Chorismate_bind.
DR Pfam; PF00425; Chorismate_bind; 1.
DR PRINTS; PR00095; ANTSNTHASEI.
DR PRODOM; PD000779; Chorismate_bind; 1.
KW Tryptophan biosynthesis; Lyase; Complete proteome.
SQ SEQUENCE 411 AA; 46346 MW; 2D65F91E5BF4457A CRC64;

Query Match 78.4%; Score 29; DB 1; Length 411;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6
Db 5 EYVNPV 10
|||||

RESULT 10
GAG2_DROME
ID GAG2_DROME STANDARD; PRT; 414 AA.
AC P20828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE RETROVIRUS-RELATED GAG POLYPROTEIN (TRANSPONSON 297).
GN GAG.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86108354; PubMed=2417839;
RA Inoue S., Yuki S., Saigo K.;
RT "Complete nucleotide sequence and genome organization of a Drosophila
transposable genetic element, 297.";
RL Eur. J. Biochem. 154:417-425(1986).
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CC -----
DR EMBL; X03431; CAA27159.1; -
DR PIR; A24872; A24872.
DR FlyBase; FBgn0000005; 297.
KW Core protein; Polyprotein; Transposable element.
SQ SEQUENCE 414 AA; 49250 MW; 7393C9CEEB864148 CRC64;

Query Match 78.4%; Score 29; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINP 5
Db 274 QYINP 278
|||||

RESULT 11
YAS2_SCHPO STANDARD; PRT; 444 AA.
AC Q10138;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 51.5 KDA PROTEIN C3H8.02 IN CHROMOSOME 1.
GN SPAC3H8.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; Z69086; CAA93159.1; -
DR InterPro; IPR001251; CRAL-TRIO.
DR Pfam; PF00650; CRAL-TRIO; 1.
DR SMART; SM00516; SEC14; 1.
KW Hypothetical protein.
FT DOMAIN 52 57 POLY-SER.
SQ SEQUENCE 444 AA; 51473 MW; 95C4DC7AE5A2E27D CRC64;

Query Match 78.4%; Score 29; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QYINP 5
Db 311 QYINP 315
|||||

RESULT 12
YBXG_BACSU STANDARD; PRT; 462 AA.
ID YBXG_BACSU
AC P54425; O31438;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL TRANSPORT PROTEIN IN NDHF-CSGA INTERGENIC REGION (ORF1).
GN YBXG OR YBDP.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
RT "Sequence analysis of the 70kb region between 17 and 23 degree of the
Bacillus subtilis chromosome.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC [2]
CC SEQUENCE OF 339-462 FROM N.A.
RC STRAIN=168 / PY79;
RX MEDLINE=97169156; PubMed=9016963;
RA Scheplov M., Chyu G., Bagyan I., Cutting S.M.;
RT "Characterization of csGA, a new member of the forespore-expressed
sigmaG-regulon from Bacillus subtilis.";
RL Gene 184:133-140(1997).
CC -!- FUNCTION: PROBABLE AMINO-ACID OR METABOLITE TRANSPORT PROTEIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
CC -----
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CC -----
DR EMBL; AB006424; BAA33104.1; -
DR EMBL; X92859; CAA63442.1; -
DR EMBL; Z99105; CAB12000.1; -
DR Subtilist; BG11505; ybxG.
DR InterPro; IPR002293; AA_rel_permease_1.
DR InterPro; IPR002027; Amino_acid_permease.
DR Pfam; PF00324; aa_permeases; 1.
DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
Complete proteome.
FT TRANSMEM 17 37 POTENTIAL.
FT TRANSMEM 38 58 POTENTIAL.
FT TRANSMEM 89 109 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 190 210 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 276 296 POTENTIAL.
FT TRANSMEM 331 351 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
FT TRANSMEM 398 418 POTENTIAL.
FT TRANSMEM 427 447 POTENTIAL.
FT TRANSMEM 339 363 POTENTIAL.
FT CONFLICT
SQ SEQUENCE 462 AA; 50109 MW; CACC1787D650952C CRC64;

Query Match 78.4%; Score 29; DB 1; Length 462;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
||:|:|
DB 80 QYIHMA 86

RESULT 13
ID YBP4_YEAST STANDARD; PRT; 525 AA.
AC P34219;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 59.2 KDA PROTEIN IN PTC3-SAS3 INTERGENIC REGION.
GN YBL054W OR YBL0513 OR YBL0509.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94205266; PubMed=8154187;
RA Scherens B., el Bakkoury M., Vlerendeels F., Dubois E., Messenguy F.;
RT "Sequencing and functional analysis of a 32,560 bp segment on the
left arm of yeast chromosome II. Identification of 26 open reading
frames, including the KIP1 and SEC17 genes.";
RL Yeast 9:1355-1371(1993).
CC -1- SIMILARITY: STRONG, TO YEAST YER088C.

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CC EMBL; 23261; CAA80793.1; -;
DR EMBL; 235815; CAA84874.1; -;
DR PIR; S39834; S39834.
DR PIR; S37335; S37335.
DR HSP; P06876; IMBF.
DR SGD; S0000150; YBL054W.
DR InterPro; IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-Binding; 1.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS50090; MYB_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 525 AA; 59226 MW; 8663DFE2641AA72E CRC64;

Query Match 78.4%; Score 29; DB 1; Length 525;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7
||:|:|
DB 360 YLNPIA 365

RESULT 14
ID TEX_BORPE STANDARD; PRT; 791 AA.
AC Q45388;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TEX PROTEIN.

GN Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOHAMA I;
RX MEDLINE=96345608; PubMed=8755871;
RA Fuchs T.M., Deppisch H., Scarlato V., Gross R.;
RT "A new gene locus of Bordetella pertussis defines a novel family of
prokaryotic transcriptional accessory proteins.";
RL J. Bacteriol. 178:4445-4452(1996).
CC -1- FUNCTION: TRANSCRIPTION ACCESSORY PROTEIN. EXACT FUNCTION NOT
KNOWN.
CC -1- SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.

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CC EMBL; X95386; CAA64672.1; -;
DR HSP; P05055; LSRO.
DR InterPro; IPR003029; S1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
KW RNA-binding.
FT DOMAIN 670 739 S1 MOTIF.
SQ SEQUENCE 791 AA; 85727 MW; F5185AB010294FFD CRC64;

Query Match 78.4%; Score 29; DB 1; Length 791;
Best Local Similarity 71.4%; Pred. No. 14e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
||:|:|
DB 157 QYLNPEA 163

RESULT 15
ID T2D2_YEAST STANDARD; PRT; 1407 AA.
AC P23255;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE TRANSCRIPTION INITIATION FACTOR TFIID 150 KDA SUBUNIT (TAFII-150)
(TSM1 PROTEIN) (TSM-1).
GN TSM1 OR TAF150 OR YCR042C OR YCR42C OR YCR724.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92160397; PubMed=1789011;
RA Jacquet M., Buhler J.-M., Iborra F., Francinguet-Gaillard M.-C.,
RA Soustelle C.;
RT "The MAT locus revisited within a 9.8 kb fragment of chromosome III
containing BUD5 and two new open reading frames.";
RL Yeast 7:881-888(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RY570;
RX MEDLINE=92035068; PubMed=1840512;
RA Ray B.L., White C.I., Haber J.E.;
RT "The TSM1 gene of Saccharomyces cerevisiae overlaps the MAT locus.";
RL Curr. Genet. 20:25-31(1991).

[3]
RN SEQUENCE OF 165-174 AND 991-1000, AND CHARACTERIZATION.
RP STRAIN-YPH252;
RX MEDLINE-95396770; PubMed-7667272;
RA Poon D., Bai Y., Campbell A.M., Bjorklund S., Kim Y.-J., Zhou S.,
RA Kornberg R.D., Weil P.A.;
RT "Identification and characterization of a TFIID-like multiprotein
RL complex from Saccharomyces cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:8224-8228(1995).
CC -!- FUNCTION: TAFs ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID
CC (TFIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF
CC RNA POLYMERASE TRANSCRIPTION.
CC -!- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs) WHOSE MW RANGE FROM
CC 25-150 KDA.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: TO DROSOPHILA TAFII-150.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63853; CAA45337.1; -;
DR EMBL; M60486; AAA35179.1; -;
DR EMBL; X59720; CAA42200.1; -;
DR PIR; S19455; BWHYMI.
DR SGD; S0000638; TSM1.
KW Transcription regulation; Nuclear protein.
FT DOMAIN 259 334 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1285 1350 HIGHLY CHARGED.
FT CONFLICT 323 323 E -> G (IN REF. 2).
SQ SEQUENCE 1407 AA; 161470 MW; 184C8ED735443F38 CRC64;

Query Match 78.4%; Score 29; DB 1; Length 1407;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QYINPVA 7
Db 370 QIINPVA 376

Search completed: March 9, 2002, 00:47:38
Job time: 799 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:53 ; Search time 94.88 Seconds
(without alignments)
10.792 Million cell updates/sec

Title: US-09-922-067-10
Perfect score: 37
Sequence: 1 QYINPVA 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_nhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	86.5	341	10 Q9XGV4	Q9xgv4 brassica na
2	32	86.5	441	10 Q9SLD2	Q9sls2 arabidopsis
3	32	86.5	501	10 Q9M4V2	Q9m4v2 brassica na
4	32	86.5	503	10 Q9XGR5	Q9xgr5 brassica na
5	32	86.5	520	10 Q9S7P2	Q9s7p2 arabidopsis
6	32	86.5	532	10 Q9SEG9	Q9seg9 nicotiana t
7	32	86.5	534	10 Q9FUL6	Q9ful6 perilla fru
8	31	83.8	349	5 Q9GRX8	Q9grx8 chironomus
9	31	83.8	513	3 Q9P8X7	Q9p8x7 aspergillus
10	31	83.8	519	5 Q9W131	Q9w131 drosophila
11	31	83.8	747	5 Q24746	Q24746 drosophila
12	31	83.8	764	3 Q42976	Q42976 schizosacch
13	31	83.8	771	2 P71602	P71602 mycobacteri
14	31	83.8	884	4 Q9UPX6	Q9upx6 homo sapien
15	31	83.8	1417	2 Q9HWR8	Q9hwr8 pseudomonas
16	31	83.8	1498	3 Q9P884	Q9p884 emericeilla
17	30	81.1	149	2 P73048	P73048 synecocyst
18	30	81.1	178	13 Q93594	Q93594 dicentrarch
19	30	81.1	219	13 Q91036	Q91036 gadus morhu

20 30 81.1 237 13 Q91515
21 30 81.1 238 13 Q9W7Q6
22 30 81.1 240 13 Q98TH0
23 30 81.1 242 13 Q9W7Q7
24 30 81.1 248 2 Q45033
25 30 81.1 347 2 Q9S3U6
26 30 81.1 420 5 Q17324
27 30 81.1 698 2 Q9KUZ7
28 30 81.1 753 5 Q36306
29 30 81.1 1547 3 Q9C1A0
30 29 78.4 76 5 Q24505
31 29 78.4 154 10 Q41287
32 29 78.4 173 2 Q9F3U2
33 29 78.4 180 12 Q9J5H3
34 29 78.4 189 2 Q99T66
35 29 78.4 235 5 Q17378
36 29 78.4 243 12 Q9E046
37 29 78.4 243 12 Q9E045
38 29 78.4 243 12 Q9E044
39 29 78.4 243 12 Q9E043
40 29 78.4 243 12 Q9E042
41 29 78.4 295 10 Q82796
42 29 78.4 295 10 Q9F285
43 29 78.4 364 5 Q9VXJ5
44 29 78.4 411 10 Q46322
45 29 78.4 421 2 Q9KTA2

ALIGNMENTS

RESULT 1

Q9XGV4 PRELIMINARY; PRT; 341 AA.
AC Q9XGV4;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).
GN DGAT2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, JET NEUF;
RA Nykiforuk C.L., Larocche A., Weselake R.J.;
RT "A novel full length cDNA exhibiting high homology to diacylglycerol
acyltransferase (DGAT) in a microspore-derived cell suspension culture
from Brassica napus cv. Jet Neuf.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF155224; AAD40881.1;
DR InterPro: IPR002688; ACAT.
DR Pfam: PF01800; ACAT; 1
KW Transferase; Acyltransferase.
SQ SEQUENCE 341 AA; 39532 MW; 1A46340C49F16332 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 341;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QYINPV 6
|||||
Db 152 QYINPI 157

RESULT 2

Q9SLD2 PRELIMINARY; PRT; 441 AA.
AC Q9SLD2;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE DIACYLGLYCEROL O-ACYLTRANSFERASE.
 GN AT2G19450.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";
 RL Nature 402:761-768(1999).
 DR EMBL: AC005917; RAD10144.1; -;
 DR InterPro: IPR002688; ACAT.
 DR Pfam: PF01800; ACAT; 1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 441 AA; 49614 MW; 9E13D1C70539182F CRC64;

Query Match 86.5%; Score 32; DB 10; Length 441;
 Best Local Similarity 83.3%; Pred. No. 79;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
 |||||
 Db 269 QYINPI 274

RESULT 3
 Q9M4V2
 ID Q9M4V2 PRELIMINARY; PRT; 501 AA.
 AC Q9M4V2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COMMANCHE;
 RA Brown A.P., Schierer T.P., Slabas A.R.;
 RT "Characterization of a putative diacylglycerol acyltransferase cDNA
 from Brassica napus embryo.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF251794; AAF64065.1; -;
 DR InterPro: IPR002688; ACAT.
 DR Pfam: PF01800; ACAT; 1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 501 AA; 57538 MW; 29E022B278D60822 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 501;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
 |||||
 Db 312 QYINPI 317

RESULT 4
 Q9XGR5
 ID Q9XGR5 PRELIMINARY; PRT; 503 AA.
 AC Q9XGR5;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PUTATIVE DIACYLGLYCEROL ACYLTRANSFERASE (EC 2.3.1.20).
 GN DGAT1.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CULTIVAR JET NEUF;
 RA Nykiforuk C.L., Laroche A., Weselake R.J.;
 RT "A cDNA exhibiting high homology to diacylglycerol acyltransferase
 (DGAT) in a microspore-derived cell suspension culture from Brassica
 napus cv. Jet Neuf.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF164434; AAD45536.1; -;
 DR InterPro: IPR002688; ACAT.
 DR Pfam: PF01800; ACAT; 1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 503 AA; 56931 MW; 2B578A16FE0AD758 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 503;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYINPV 6
 |||||
 Db 314 QYINPI 319

RESULT 5
 Q9S7F2
 ID Q9S7F2 PRELIMINARY; PRT; 520 AA.
 AC Q9S7F2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE DIACYLGLYCEROL ACYLTRANSFERASE.
 GN DGAT OR DAGAT.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
 RX MEDLINE=20069349; PubMed=10601854;
 RA Bouvier-Nave P., Benveniste P., Oelkers P., Sturley S.L., Schaller H.;
 RT "Expression in yeast and tobacco of plant cDNAs encoding acyl
 CoA:diacylglycerol acyltransferase.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
 RX MEDLINE=20069349; PubMed=10601854;
 RA Bouvier-Nave P., Benveniste P., Oelkers P., Sturley S.L., Schaller H.;
 RT "Expression in yeast and tobacco of plant cDNAs encoding acyl
 CoA:diacylglycerol acyltransferase.";
 RL Eur. J. Biochem. 267:85-96(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
 RX MEDLINE=99313150; PubMed=10386579;
 RA Hills M.J., Lu C., Hobbs D.H.;
 RT "Cloning of a cDNA encoding diacylglycerol acyltransferase from

RT Arabidopsis thaliana and its functional expression. ;
RL FEBS Lett. 452:145-149(1999).
DR EMBL; AJ238008; CAB45373.1; -;
DR EMBL; AF051849; AAF19262.1; -;
DR EMBL; AJ131831; CAB44774.1; -;
DR InterPro; IPR002688; ACAT.
DR Pfam; PF01800; ACAT; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 520 AA; 58985 MW; 9CD0E3E956CEFF4 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 520;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6
|||||
Db 331 QYINPI 336

RESULT 6
Q9SEG9 PRELIMINARY; PRT; 532 AA.
ID Q9SEG9
AC Q9SEG9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DIACYLGLYCEROL ACYLCOA ACYLTRANSFERASE.
GN DAGAT.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI SH6; TISSUE=CALLI DERIVED FROM LEAF PROTOPLASTS;
RX MEDLINE=20069349; Pubmed=10601854;
RA Bouvier-Nave P., Benveniste P., Oelkers P., Sturley S.L., Schaller H.;
RT "Expression in yeast and tobacco of plant cDNAs encoding acyl
CoA:diacylglycerol acyltransferase. ;
RL Eur. J. Biochem. 267:85-96(2000).
DR EMBL; AF129003; AAF19345.1; -;
DR InterPro; IPR002688; ACAT.
DR Pfam; PF01800; ACAT; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 532 AA; 60867 MW; C9D316E7A8799310 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 532;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6
|||||
Db 342 QYINPI 347

RESULT 7
Q9FUL6 PRELIMINARY; PRT; 534 AA.
ID Q9FUL6
AC Q9FUL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DIACYLGLYCEROL ACYLTRANSFERASE.
GN DGATI.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]

RT Arabidopsis thaliana and its functional expression. ;
RL FEBS Lett. 452:145-149(1999).
DR EMBL; AJ238008; CAB45373.1; -;
DR EMBL; AF051849; AAF19262.1; -;
DR EMBL; AJ131831; CAB44774.1; -;
DR InterPro; IPR002688; ACAT.
DR Pfam; PF01800; ACAT; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 520 AA; 58985 MW; 9CD0E3E956CEFF4 CRC64;

RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG;
RA Hwang S., Hwang Y.;
RT "Isolation of Perilla frutescens diacylglycerol acyltransferase
cDNA. ;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF298815; AAG23696.1; -;
DR InterPro; IPR002688; ACAT.
DR Pfam; PF01800; ACAT; 1.
KW Transferase; Acyltransferase.
SQ SEQUENCE 534 AA; 61205 MW; 8FEC173E06E5BB70 CRC64;

Query Match 86.5%; Score 32; DB 10; Length 534;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6
|||||
Db 344 QYINPI 349

RESULT 8
Q9GRX8 PRELIMINARY; PRT; 349 AA.
ID Q9GRX8
AC Q9GRX8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RAE1.
GN RAE1.
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]

RP SEQUENCE FROM N.A.
RA Sabri N., Visa N.;
RT "Interaction of Ct-RAE1 with Balbiani ring RNP particles during
nuclear export occurs at the nuclear pore. ;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AJ277787; CAC14665.1; -;
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS0082; WD_REPEATS_2; 3.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 349 AA; 39322 MW; EF475B9EEDC19411 CRC64;

Query Match 83.8%; Score 31; DB 5; Length 349;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPV 6
|||||
Db 227 QYINPV 232

RESULT 9
Q9P8X7 PRELIMINARY; PRT; 513 AA.
ID Q9P8X7
AC Q9P8X7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEXOSE TRANSPORTER PROTEIN.
GN HXTA.
OS Aspergillus parasiticus.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SU-1;
 RA Yu J.;
 RT "Cloning of sugar utilization pathway gene cluster in Aspergillus
 parasiticus";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
 DR EMBL; AF168613; AAF26275.1; -;
 DR InterPro; IPR003662; sub-transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_2.
 KW Transmembrane.
 SQ SEQUENCE 513 AA; 55986 MW; 0C7EDF709AD7DAA5 CRC64;

Query Match 83.8%; Score 31; DB 3; Length 513;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 I:|||||
 Db 430 QVNPPIA 436

RESULT 10
 Q9W131
 ID Q9W131 PRELIMINARY; PRT; 519 AA.
 AC Q9W131;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CG13594 PROTEIN (FRAGMENT).
 GN CG13594.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari P., Brottier P.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos L., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003464; AAF47246.1; -;
 DR FlyBase; FBgn0035041; CG13594.
 FT NON_TER 519
 SQ SEQUENCE 519 AA; 53915 MW; F9B3C22A61245D3B CRC64;

Query Match 83.8%; Score 31; DB 5; Length 519;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YINPVA 7
 I:|||||
 Db 219 YVNPVA 224

RESULT 11
 Q24746
 ID Q24746 PRELIMINARY; PRT; 747 AA.
 AC Q24746;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE NEURALIZED PROTEIN.
 GN NEUR OR NEU.
 OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95095077; PubMed=8001814;
 RA Zhou L., Boulianne G.L.;
 RT "Comparison of the neuralized genes of Drosophila virilis and D.
 RT melanogaster.";
 RL Genome 37:840-847(1994).
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL; U12593; AAB60619.1; -;
 DR EMBL; U12591; AAB60619.1; JOINED.
 DR EMBL; U12592; AAB60619.1; JOINED.
 DR FlyBase; FBgn0013132; Dvir\neur.
 DR InterPro; IPR001841; ZnF_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 747 AA; 81982 MW; C8E72569D6FDCALL CRC64;

Query Match 83.8%; Score 31; DB 5; Length 747;
 Best Local Similarity 85.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 I:|||||
 Db 561 QYIEPVA 667

RESULT 12
 Q42976
 ID Q42976 PRELIMINARY; PRT; 764 AA.
 AC Q42976;

DT 01-JAN-1999 (TrEMBLrel. 09, Created)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HYPOTHETICAL 85.4 KDA PROTEIN C20F10.07 IN CHROMOSOME II.
 GN SPBC20F10.07.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne W., McDougall R., Rajandream M.A., Barrell B.G., Beck A.,
 RA Reinhardt R.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: SOME, TO YEAST YHR080C.
 DR EMBL; AL021747; CAA16847.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 764 AA; 85354 MW; 080990E5C7F4A7B2 CRC64;

Query Match 83.8%; Score 31; DB 3; Length 764;
 Best Local Similarity 85.7%; Pred. NO. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QYINPVA 7

Db 489 QYIKPVA 495

RESULT 13
 P71602 PRELIMINARY; PRT; 771 AA.
 ID P71602
 AC P71602;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 86.2 KDA PROTEIN CY10H4.32.
 GN RV0032 OR MTCY10H4.32.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL; Z80233; CAB02417.1; -;
 DR HSSP; P12998; IBS0.
 DR TubercuList; Kv0032; -;
 DR InterPro; IPR001917; Aminotransf_2.
 DR Pfam; PF00222; aminotran_2; 1.
 DR PROSITE; PS00599; AA.TRANSFER_CLASS_2; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 771 AA; 86242 MW; 8FC1D0FED27E43C6 CRC64;

Query Match 83.8%; Score 31; DB 2; Length 771;
 Best Local Similarity 83.3%; Pred. NO. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YINPVA 7

Db 721 YVNPVA 726

RESULT 14

OY Q9UPX6 PRELIMINARY; PRT; 884 AA.

AC Q9UPX6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE KIAA1024 PROTEIN (FRAGMENT).
 GN KIAA1024.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99397452; PubMed=10470851;
 RX Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205(1999).
 DR EMBL; AB028947; BAA82976.1; -;
 DR InterPro; IPR002106; AA_TRNA_LIGASE_II.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 FT NON_TER
 SQ SEQUENCE 884 AA; 99289 MW; 4594A37B0CF3C7B4 CRC64;

Query Match 83.8%; Score 31; DB 4; Length 884;
 Best Local Similarity 83.3%; Pred. NO. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYINPV 6

Db 279 QYLNVP 284

RESULT 15
 Q9HWR8 PRELIMINARY; PRT; 1417 AA.
 ID Q9HWR8
 AC Q9HWR8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PROBABLE SENSOR/RESPONSE REGULATOR HYBRID.
 GN PA4112.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS
 CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
 CC KINASES.
 DR EMBL; AE004827; AAG07499.1; -;
 DR InterPro; IPR000410; Bctrl_sense.
 DR InterPro; IPR003594; HATPase_c.
 DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR002570; Hpt.
 DR InterPro; IPR001610; PAC.
 DR InterPro; IPR000014; PAS.

DR InterPro; IPR000700; PAS-assoc_C.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00785; PAC; 3.
 DR Pfam; PF00989; PAS; 2.
 DR Pfam; PF00072; response_reg; 2.
 DR Pfam; PF00512; signal; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; Hiska; 1.
 DR SMART; SM00073; HPT; 1.
 DR SMART; SM00086; PAC; 3.
 DR SMART; SM00091; PAS; 3.
 DR SMART; SM00448; REC; 2.
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW Transferrase.
 SQ SEQUENCE 1417 AA; 153893 MW; 224E2EC9E45EAF2B CRC64;

Query Match 83.8%; Score 31; DB 2; Length 1417;
 Best Local Similarity 85.7%; Pred. No. 5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYINPVA 7
 |||||
 Db 147 QYIEPVA 153

Search completed: March 9, 2002, 00:46:55
 Job time: 831 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:31:57 ; Search time 114.5 Seconds
(without alignments)
12.939 Million cell updates/sec

Title: US-09-922-067-11
Perfect score: 104
Sequence: 1 MITIRSVHQNFADFTFATG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*

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22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	104	100.0	20	AAR64930	Human lipoprotein-
2	104	100.0	27	AAR64929	Human lipoprotein-
3	104	100.0	440	AAE00782	Mouse-Human plasma
4	104	100.0	440	AAE00783	Mouse-Human plasma
5	104	100.0	441	AAR73048	Human acetyl hydro
6	104	100.0	441	AAR73049	Human acetyl hydro
7	104	100.0	441	AAR73050	Human acetyl hydro
8	104	100.0	441	AAR71920	Human acetyl hydro
9	104	100.0	441	AAR71921	Human acetyl hydro
10	104	100.0	441	AAR71922	Human acetyl hydro
11	104	100.0	441	AAR71923	Human acetyl hydro

12	104	100.0	441	16	AAR71925	Human acetyl hydro
13	104	100.0	441	16	AAR73046	Human acetyl hydro
14	104	100.0	441	16	AAR73047	Human acetyl hydro
15	104	100.0	441	16	AAR71913	Human plasma plate
16	104	100.0	441	18	AAW26498	Human platelet-act
17	104	100.0	441	18	AAW23796	Human plasma plate
18	104	100.0	441	18	AAW09808	Platelet-activatin
19	104	100.0	441	19	AAW38361	Human plasma plate
20	104	100.0	441	20	AAW96334	Human plasma plate
21	104	100.0	441	20	AAW73359	Human PAF-AH prote
22	104	100.0	441	21	AAW07774	Plasma platelet-ac
23	104	100.0	441	21	AAW07774	Human low density
24	104	100.0	441	21	AAW07774	Human platelet-act
25	104	100.0	441	21	AAW07774	Human PAF-AH prote
26	104	100.0	441	22	AAW07774	Human plasma plate
27	104	100.0	441	22	AAW07774	Human plasma plate
28	104	100.0	441	22	AAW07774	Human plasma plate
29	104	100.0	441	22	AAW07774	Human plasma plate
30	104	100.0	441	22	AAW07774	Human plasma plate
31	104	100.0	441	22	AAW07774	Human plasma plate
32	104	100.0	441	22	AAW07774	Human plasma plate
33	104	100.0	441	22	AAW07774	Human platelet-act
34	104	100.0	441	22	AAW07774	Human plasma plate
35	104	100.0	441	22	AAW07774	Human plasma plate
36	104	100.0	441	22	AAW07774	Human plasma plate
37	104	100.0	441	22	AAW07774	Human plasma plate
38	104	100.0	441	22	AAW07774	Human plasma plate
39	104	100.0	441	22	AAW07774	Human plasma plate
40	104	100.0	441	22	AAW07774	Human plasma plate
41	104	100.0	441	22	AAW07774	Human plasma plate
42	100	96.2	444	16	AAW4928	Human T-cell lymph
43	100	96.2	444	16	AAW71915	Canine platelet ac
44	100	96.2	444	18	AAW26501	Canine platelet-ac
45	100	96.2	444	18	AAW23798	Canine plasma plat
				18	AAW09810	Canine platelet-ac

ALIGNMENTS

RESULT 1

AAR64930

ID AAR64930 standard; Peptide; 20 AA.

AC AAR64930;

XX

XX 18-AUG-1995 (first entry)

DT

XX Human lipoprotein-associated phospholipase-A2 peptide-6.

DE

XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;

KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.

KW

XX Homo sapiens.

OS

XX WO9500649-A.

PN

XX

XX 05-JAN-1995.

PD

XX

XX 24-JUN-1994; 94WO-GB01374.

PF

XX

XX 25-JUN-1993; 93GB-0013144.

PR

XX 11-JAN-1994; 94GB-0000413.

XX

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX

XX Gloger IS, Hickey DMB, Lawrence GMP, Macphree CH;

XX Rice SQJ, Southan CD, Tew DG;

XX

XX WPI; 1995-052086/07.

XX

XX Purified lipoprotein associated phospholipase A2 - used to

PT develop prods. for diagnosis and therapy, partic. inhibitors for

PT treatment of atherosclerosis

XX Claim 9; Page 21; 29pp; English.

XX This sequence encodes a peptide fragment of an enzyme which may be
 CC used in a method of screening compounds to identify those compounds
 CC which inhibit Lp-PLA2 which involves contacting isolated Lp-PLA2
 CC with a test compound and measuring the rate of turnover of an
 CC enzyme substrate as compared with the rate of turnover in the
 CC absence of the test compound.

XX Sequence 20 AA;

Query Match 100.0%; Score 104; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.2e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAADFTFATG 20
 Db 1 mitirgsvhqnfnadftfatg 20

RESULT 2

AAR64929
 ID AAR64929 standard; Peptide; 27 AA.

AC AAR64929;

DT 18-AUG-1995 (first entry)

DE Human lipoprotein-associated phospholipase-A2 peptide-3.

XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2;
 KW enzyme; atherosclerosis; diagnosis; therapy; antiarteriosclerotic.

XX Homo sapiens.

XX WO9500649-A.

XX 05-JAN-1995.

XX 24-JUN-1994; 94WO-GB01374.

XX 25-JUN-1993; 93GB-0013144.

XX 11-JAN-1994; 94GB-0000413.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Gloger IS, Hickey DMB, Lawrence GMP, Macphree CH;

XX Rice SQJ, Southan CD, Tew DG;

XX WPI; 1995-052086/07.

XX Purified lipoprotein-associated phospholipase A2 - used to
 PT develop prods. for diagnosis and therapy, partic. inhibitors for
 PT treatment of atherosclerosis

XX Claim 9; Page 17; 29pp; English.

XX This sequence encodes a peptide fragment of an enzyme which may be
 CC used in a method of screening compounds to identify those compounds
 CC which inhibit Lp-PLA2 which involves contacting isolated Lp-PLA2
 CC with a test compound and measuring the rate of turnover of an
 CC enzyme substrate as compared with the rate of turnover in the
 CC absence of the test compound.

XX Sequence 27 AA;

Query Match 100.0%; Score 104; DB 16; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAADFTFATG 20
 Db 8 mitirgsvhqnfnadftfatg 27

RESULT 3

AAR60782

ID AAR60782 standard; Protein; 440 AA.

XX AAE00782;

XX 02-JUL-2001 (first entry)

DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHCl.

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

XX Key Location/Qualifiers
 FH 1..97

FT /note= "Corresponds to N-terminal 97 amino acids of mouse
 FT plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"

FT 98..440

FT /note= "Corresponds to C-terminal 343 amino acids of
 FT human plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"

XX US6203790-B1.

XX 20-MAR-2001.

XX 23-MAY-2000; 2000US-0577758.

XX 07-JUN-1995; 95US-0480658.

XX 22-JAN-1998; 98US-0010715.

XX 06-OCT-1993; 93US-0133803.

XX 06-OCT-1994; 94US-0318905.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;

XX WPI; 2001-280610/29.

XX N-PSDB; AAD04168.

XX Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF -

XX Example 8; Column -; 54pp; English.

XX The present sequence is mouse-human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHCl.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
 CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 SQ Sequence 440 AA;
 Query Match 100.0%; Score 104; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MITIRGSVHQNFAFTFATG 20
 ||||||||||||||||
 Db 342 mitirgsvhqnfdftfatg 361
 RESULT 4
 AA00783
 ID AAE00783 standard; Protein: 440 AA.
 XX
 AC AAE00783;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.
 XX
 KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..40
 FT /note= "Corresponds to N-terminal 40 amino acids of mouse
 FT plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 FT Region 41..440
 FT /note= "Corresponds to C-terminal 400 amino acids of
 FT human plasma platelet-activating factor acetylhydrolase
 FT (PAF-AH)"
 XX
 US6203790-B1.
 XX
 20-MAR-2001.
 XX
 23-MAY-2000; 2000US-0577758.
 XX
 07-JUN-1995; 95US-0480658.
 XX
 22-JAN-1998; 98US-0010715.
 XX
 06-OCT-1993; 93US-0133803.
 XX
 06-OCT-1994; 94US-0318905.
 XX
 (ICOS-) ICOS CORP.
 XX
 Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX
 WPI; 2001-280610/29.
 DR N-PSDB; AAD04169.
 XX
 Treating a mammal susceptible to or suffering from septicemia comprises
 PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
 PT supplement endogenous PAF-AH activity and to inactivate pathological
 PT amounts of PAF -
 XX
 Example 8; Column -: 54pp; English.
 PS
 XX The present sequence is mouse-human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid
 CC pRC/PH.MHC2.
 CC The invention relates to human plasma platelet-activating factor
 CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to
 CC or suffering from septicemia. PAF functions in normal physiological
 CC processes such as inflammation, haemostasis and parturition. PAF-AH
 CC specific antibodies are used in the diagnostic methods to detect abnormal
 CC levels of PAF-AH in serum and also for treating the pathological
 CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
 CC shock and arthritis. PAF-AH antibody is also useful for screening a
 CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
 CC replacement of nucleotide G to T at position 996 within exon 9 resulting
 CC in replacement of amino acid Val to Phe at position 279. Thus the
 CC deficiency of PAF-AH activity is due to the genetic lesion in human
 CC plasma PAF-AH gene.
 XX
 SQ Sequence 440 AA;
 Query Match 100.0%; Score 104; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 4.1e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MITIRGSVHQNFAFTFATG 20
 ||||||||||||||||
 Db 342 mitirgsvhqnfdftfatg 361
 RESULT 5
 AAR73048
 ID AAR73048 standard; Protein: 441 AA.
 XX
 AC AAR73048;
 XX
 DT 06-DEC-1995 (first entry)
 XX
 DE Human acetyl hydrolase (AH) mutant C291S.
 XX
 KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 291
 FT /note= "Wild-type Cys is substd. by Ser."
 FT
 XX
 W09509921-A.
 XX
 13-APR-1995.
 XX
 06-OCT-1994; 94WO-US11340.
 XX
 06-OCT-1993; 93US-0133803.
 XX
 (ICOS-) ICOS CORP.
 XX
 Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;
 XX
 WPI; 1995-155262/20.
 XX
 New nucleic acid encoding platelet activating factor,
 PT acetylhydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy
 XX
 Example 10; : 80pp; English.
 PS
 XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The

CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
 |||||
 Db 343 mitirgsvhqnfdftfatg 362

RESULT 6

AAR73049
 ID AAR73049 standard; Protein; 441 AA.

AC AAR73049;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C334S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 334 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

PR 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
 |||||
 Db 343 mitirgsvhqnfdftfatg 362

RESULT 7

AAR73050
 ID AAR73050 standard; Protein; 441 AA.

AC AAR73050;

DT 06-DEC-1995 (first entry)

DE Human acetyl hydrolase (AH) mutant C407S.

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 407 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

PR 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
 PT acetyl:hydrolase - useful in diagnosis and for treating
 PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these mutants are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
 |||||
 Db 343 mitirgsvhqnfdftfatg 362

RESULT 8

AAR71920
 ID AAR71920 standard; Protein; 441 AA.

XX AAR71920;

XX 06-DEC-1995 (first entry)
DT Human acetyl hydrolase (AH) mutant S108A.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 108
FT /note= "Wild-type Ser is substd. by Ala."
XX
XX WO9509921-A.
PN
XX 13-APR-1995.
PD
XX 06-OCT-1994; 94WO-US11340.
PF
XX 06-OCT-1993; 93US-0133803.
PR
XX (ICOS-) ICOS CORP.
PA
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
PI
XX WPI: 1995-155262/20.
DR
XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
XX
XX Example 10; : 88pp; English.
PS
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;
Query Match 100.0%; Score 104; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITIRGSHVHQNFAFTFTATG 20
Db ||||||||||||||||
343 mitirgshvhnqnfadftfatg 362
RESULT 9
AAR71921
ID AAR71921 standard; Protein; 441 AA.
XX
XX AAR71921;
XX
XX 06-DEC-1995 (first entry)
DT
XX Human acetyl hydrolase (AH) mutant S273A.
DE
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
OS
XX

FH Key Location/Qualifiers
FT Misc-difference 273
FT /note= "Wild-type Ser is substd. by Ala."
XX
XX WO9509921-A.
PN
XX 13-APR-1995.
PD
XX 06-OCT-1994; 94WO-US11340.
PF
XX 06-OCT-1993; 93US-0133803.
PR
XX (ICOS-) ICOS CORP.
PA
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
PI
XX WPI: 1995-155262/20.
DR
XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy
XX
XX Example 10; : 88pp; English.
PS
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).
CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.
XX
XX Sequence 441 AA;
Query Match 100.0%; Score 104; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MITIRGSHVHQNFAFTFTATG 20
Db ||||||||||||||||
343 mitirgshvhnqnfadftfatg 362
RESULT 10
AAR71922
ID AAR71922 standard; Protein; 441 AA.
XX
XX AAR71922;
XX
XX 06-DEC-1995 (first entry)
DT
XX Human acetyl hydrolase (AH) mutant D296A.
DE
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 296
FT /note= "Wild-type Asp is substd. by Ala."
FT
XX WO9509921-A.
PN
XX 13-APR-1995.
PD
XX 06-OCT-1994; 94WO-US11340.
PF
XX

PR 06-OCT-1993; 93US-0133803.

PA (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 4.2e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAFFTATG 20

|||||

Db 343 mitirgsvhqnfaftatg 362

RESULT 11

AAR71923

ID AAR71923 standard; Protein; 441 AA.

XX AAR71923;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant D338A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 338

FT /note= "Wild-type Asp is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

PT

PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying
CC the active site of AH. The sequences of these mutants are not given
CC in the patent specification; they have been derived from the original
CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
CC gene may also be used in raising monoclonal antibodies specific for AH
CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;

Best Local Similarity 100.0%; Pred. No. 4.2e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAFFTATG 20

|||||

Db 343 mitirgsvhqnfaftatg 362

RESULT 12

AAR71925

ID AAR71925 standard; Protein; 441 AA.

XX AAR71925;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant H395A/H399A.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 395

FT /note= "Wild-type His is substd. by Ala."

FT 399

FT /note= "Wild-type His is substd. by Ala."

XX W09509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,
PT acetyl:hydrolase - useful in diagnosis and for treating
PT inflammatory diseases, e.g. pleurisy

XX Example 10; ; 88pp; English.

XX The human acetyl hydrolase (AH) gene (AA087947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying

CC the active site of AH. The sequences of these muteins are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).
 CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADFTFATG 20
 ||||||||||||||||
 Db 343 mitirgsvhqnfadftfatg 362

RESULT 13

AAR73046
 ID AAR73046 standard; Protein; 441 AA.

XX AAR73046;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C67S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 67 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

XX acetyl:hydrolase - useful in diagnosis and for treating

XX inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these muteins are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADFTFATG 20
 ||||||||||||||||
 Db 343 mitirgsvhqnfadftfatg 362

RESULT 14

AAR73047
 ID AAR73047 standard; Protein; 441 AA.

XX AAR73047;

XX 06-DEC-1995 (first entry)

XX Human acetyl hydrolase (AH) mutant C229S.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 XX disease; pleurisy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 229 /note= "Wild-type Cys is substd. by Ser."

XX WO9509921-A.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US11340.

XX 06-OCT-1993; 93US-0133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX Wilder CL;

XX WPI; 1995-155262/20.

XX New nucleic acid encoding platelet activating factor,

XX acetyl:hydrolase - useful in diagnosis and for treating

XX inflammatory diseases, e.g. pleurisy

XX Example 10; : 88pp; English.

XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 CC made with single amino acid changes for the purposes of identifying
 CC the active site of AH. The sequences of these muteins are not given
 CC in the patent specification; they have been derived from the original
 CC wild-type protein (AAR71913).

CC The AH gene and its product are useful in the treatment of inflammatory
 CC diseases, in particular pleurisy, asthma, rhinitis and eczema. The
 CC gene may also be used in raising monoclonal antibodies specific for AH
 CC that are useful in the diagnosis of such diseases.

XX Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADFTFATG 20
 ||||||||||||||||
 Db 343 mitirgsvhqnfadftfatg 362

RESULT 15
 AAR71913
 ID AAR71913 standard; Protein; 441 AA.
 XX AC AAR71913;
 XX DT 05-DEC-1995 (first entry)
 XX DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
 XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 XX KW disease; pleurisy; diagnosis.
 XX OS Homo sapiens.
 XX PN WO9509921-A.
 XX PD 13-APR-1995.
 XX PF 06-OCT-1994; 94WO-US11340.
 XX PR 06-OCT-1993; 93US-0133803.
 XX PA (ICOS-) ICOS CORP.
 XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 XX PI Wilder CL;
 XX DR WPI; 1995-155262/20.
 XX DR N-PSDB; AAQ87947.
 XX PT New nucleic acid encoding platelet activating factor,
 XX PT acetyl hydrolase - useful in diagnosis and for treating
 XX PT inflammatory diseases, e.g. pleurisy
 XX PS Claim 5; Page 53-54; 88pp; English.
 XX CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913)
 CC is useful in the treatment of inflammatory diseases, in particular
 CC pleurisy, asthma, rhinitis and eczema. The gene may also be used in
 CC raising monoclonal antibodies specific for PAF-AH that are useful in
 CC the diagnosis of such diseases.
 XX SQ Sequence 441 AA;

Query Match 100.0%; Score 104; DB 16; Length 441;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MITIRGSVHONFADFTFATG 20
 Db 343 mitirgsvhqnfdftfatg 362

Search completed: March 9, 2002, 00:31:58
 Job time: 444 sec

Query Match 100.0%; Score 104; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-12; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
|||||
DB 1 MITIRGSVHQNFADEFTFATG 20

RESULT 2

US-08-387-858A-11
; Sequence II, Application US/08387858A
; Patent No. 5981252
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858A
FILING DATE: 24 February 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994

ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-387-858A-11

Query Match 100.0%; Score 104; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-12; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
|||||
DB 1 MITIRGSVHQNFADEFTFATG 20

RESULT 3

US-09-294-384B-11
; Sequence II, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,384B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858
FILING DATE: 24 February 1995
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-09-294-384B-11

Query Match 100.0%; Score 104; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
|||||
DB 1 MITIRGSVHQNFADEFTFATG 20

RESULT 4

US-08-557-892-3
; Sequence 3, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse

APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858A
FILING DATE: 24 February 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
US-08-387-858A-3

Query Match 100.0%; Score 104; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADEFTFATG 20
Db 8 MITIRGSVHQNFADEFTFATG 27

RESULT 6
US-09-294-384B-3
Sequence 3, Application US/09294384B
Patent No. 6177257
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,384B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858
FILING DATE: 24 February 1995
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994

APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,892
FILING DATE: 14 No. 5968818ember 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,858
FILING DATE: 14 No. 5968818ember 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
US-08-557-892-3

Query Match 100.0%; Score 104; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MITIRGSVHQNFADEFTFATG 20
Db 8 MITIRGSVHQNFADEFTFATG 27

RESULT 5
US-08-387-858A-3
Sequence 3, Application US/08387858A
Patent No. 5961252
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-09-294-384B-3

Query Match 100.0%; Score 104; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
Db 8 MITIRGSVHQNFADEFTFATG 27

RESULT 7

US-08-470-187-8
Sequence 8, Application US/08470187
Patent No. 5532152

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine E.
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,187

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: No. 5532152and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31672
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-470-187-8

Query Match 100.0%; Score 104; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
Db 343 MITIRGSVHQNFADEFTFATG 362

RESULT 8

US-08-318-905-8
Sequence 8, Application US/08318905
Patent No. 5641669

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,905

FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:
NAME: No. 5641669and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-905-8

Query Match 100.0%; Score 104; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20
Db 343 MITIRGSVHQNFADEFTFATG 362

RESULT 9

US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431

GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:

; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-232-8

Query Match 100.0%; Score 104; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20

DB 343 MITIRGSVHQNFADEFTFATG 362

RESULT 10

US-08-483-140-8
; Sequence 8, Application US/08483140
; Patent No. 5638403

GENERAL INFORMATION:

; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993

ATTORNEY/AGENT INFORMATION:

; NAME: No. 5698403land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-140-8

Query Match 100.0%; Score 104; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADEFTFATG 20

DB 343 MITIRGSVHQNFADEFTFATG 362

RESULT 11

US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088

GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A

;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5847088and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32792
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-485-938A-8

Query Match 100.0%; Score 104; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADETFATG 20
|||||
DB 343 MITIRGSVHQNFADETFATG 362

RESULT 12
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rin-Laures, Li-Hsien
;; REGISTRATION NUMBER: 33,547
;; REFERENCE/DOCKET NUMBER: 27866/34026
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-910-041-8

Query Match 100.0%; Score 104; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFADETFATG 20
|||||
DB 343 MITIRGSVHQNFADETFATG 362

RESULT 13
US-09-328-474-8
; Sequence 8, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-328-474-8

Query Match 100.0%; Score 104; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
|||||
DB 343 MITIRGSVHONFADFTFATG 362

RESULT 14
US-09-100-546-8
Sequence 8, Application US/09100546
Patent No. 6099836

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 100.0%; Score 104; DB 3; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
|||||
DB 343 MITIRGSVHONFADFTFATG 362

RESULT 15
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 100.0%; Score 104; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADFTFATG 20
|||||
DB 343 MITIRGSVHONFADFTFATG 362

Search completed: March 9, 2002, 00:33:01

Mon Mar 11 10:01:54 2002

us-09-922-067-11.rai

Page 8

Job time: 402 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2002, 00:34:13 ; Search time 53.53 Seconds
(without alignments)
28.461 Million cell updates/sec

Title: US-09-922-067-11
Perfect score: 104
Sequence: 1 MITIRGSHQNFADTFATG 20
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	441	2	J60247
2	86	92.7	436	2	JC5021
3	58	55.8	384	2	T32756
4	54	51.9	476	2	T28936
5	52	50.0	541	2	T47290
6	52	50.0	830	2	T47377
7	43	41.3	341	2	T32949
8	42	40.4	142	2	B40535
9	42	40.4	325	2	A28029
10	42	40.4	374	2	S69699
11	42	40.4	1230	2	H84515
12	42	40.4	1239	2	G71266
13	41	39.4	142	2	T15957
14	41	39.4	249	2	H85786
15	41	39.4	318	1	E71690
16	41	39.4	458	2	S57605
17	41	39.4	367	2	JC4398
18	40	38.5	297	2	T27607
19	40	38.5	352	2	T49679
20	40	38.5	379	2	A49679
21	40	38.5	425	2	S75024
22	40	38.5	463	2	S77558
23	40	38.5	579	2	B44857
24	40	38.5	599	2	A46810
25	40	38.5	753	2	C96668
26	40	38.5	767	2	F64605
27	40	38.5	767	2	C71909
28	40	38.5	841	1	S24462
29	39.5	38.0	213	2	T35433

thiamin-phosphate
annexin VI - rat
hypothetical prote
hypothetical prote
hypothetical prote
probable iron-chel
intellectin - mouse
hypothetical prote
heme di biosynthes
preproteins translo
coproporphyrinogen
probable amino aci
probable MFS trans
hypothetical prote
glutamate decarbox
acetolactate synth

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 05-Nov-1999

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory

A:Reference number: S60247; MUID:95214779

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g780133

Query Match 100.0%; Score 104; DB 2; Length 441;

Best Local Similarity 100.0%; Pred. No. 4.7e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MITIRGSHQNFADTFATG 20

|||||

Db 343 MITIRGSHQNFADTFATG 362

RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 20-Jun-2000

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoy

J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating fact

A:Reference number: JC5021; MUID:97103479

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KARI>

A:Cross-references: DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:g1644229

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392

A:Experimental source: liver

C:Comment: This enzyme converts platelet-activating factor to an inactive metabolite

C:Keywords: glycoprotein; hydrolase

F:1-21/Domains: signal sequence #status predicted <SIG>

F:22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MATH>

F:76,200,324/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 82.7%; Score 86; DB 2; Length 436;
Best Local Similarity 75.0%; Pred. No. 6e-07;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAADFTFATG 20
|| :||| || |||||
Db 341 MIAVKGSVHHNFVDFTFATG 360

RESULT 3
T32756
hypothetical protein W03G9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32756
R:Dante, M.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid W03G9.
A:Reference number: Z21220
A:Accession: T32756
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-384 <DAN>
A:Cross-references: EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN000019; CESP:W03G9.6
A:Experimental source: strain Bristol N2; clone W03G9
C:Genetics:
A:Gene: CESP:W03G9.6
A:Map position: 1
A:Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 55.8%; Score 58; DB 2; Length 384;
Best Local Similarity 52.9%; Pred. No. 0.035;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAADFTF 17
::: ||||| || ||
Db 304 LUTLGAHVHQSFYDFPF 320

RESULT 4
T28936
hypothetical protein C52B9.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28936
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: Z20545
A:Accession: T28936
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-476 <NEL>
A:Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN000028; CESP:C52B9.7
A:Experimental source: strain Bristol N2; clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.7
A:Map position: x
A:Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 51.9%; Score 54; DB 2; Length 476;
Best Local Similarity 56.2%; Pred. No. 0.22;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 ITIRGSVHQNFAADFTF 17
::: ||||| || ||
Db 397 LTLNGAVHQCFSDFPF 412

RESULT 5

T47290
hypothetical protein T14K23.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47290
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24458
A:Accession: T47290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <NYA>
A:Cross-references: EMBL:AL132909
A:Experimental source: cultivar Columbia; BAC clone T14K23
C:Genetics:
A:Map position: 3
A:Introns: 109/2; 137/1; 219/1; 331/1; 365/3; 492/2
A:Note: T14K23.30

Query Match 50.0%; Score 52; DB 2; Length 541;
Best Local Similarity 44.4%; Pred. No. 0.57;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFAADFTFATG 20
::: ||||| || ||
Db 453 TVKGVHESFRDAVFALG 470

RESULT 6
T47377
hypothetical protein T5C2.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47377
R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24463
A:Accession: T47377
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-830 <OBE>
A:Cross-references: EMBL:AL138664
A:Experimental source: cultivar Columbia; BAC clone T5C2
C:Genetics:
A:Map position: 3
A:Introns: 52/3; 131/1; 171/2; 467/1; 552/1; 594/1; 710/1
A:Note: T5C2.50

Query Match 50.0%; Score 52; DB 2; Length 830;
Best Local Similarity 50.0%; Pred. No. 0.92;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFAADFTFATG 20
::: ||||| || ||
Db 57 TVKGVVHKSFDAVFALG 74

RESULT 7
T32949
hypothetical protein C05G6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32949
R:Kemp, K.
submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid C05G6.
A:Reference number: Z21252
A:Accession: T32949
A:Status: preliminary;
A:Molecule type: DNA

A:Residues: 1-341 <KEM>
A:Cross-references: EMBL:AF045635; PIDN:AA02556.1; GSPDB:GN00022; CESP:C05G6.3
A:Experimental source: strain Bristol N2; clone C05G6
C:Genetics:
A:Gene: CESP:C05G6.3
A:Map position: 4
A:Introns: 52/2; 110/1; 151/3; 195/1; 254/3; 295/3

Query Match 41.3%; Score 43; DB 2; Length 341;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 ITIRGSVHQNFAFTF 17
| | | | | | | | | |
DB 312 ISGVDVHHTFTDVT 325

RESULT 8
B40535
clathrin-associated protein 17 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 02-Mar-2001
C:Accession: B40535
J.Kirchhausen, T.; Davis, A.C.; Frucht, S.; Greco, B.O.; Payne, G.S.; Tubb, B.
J. Biol. Chem. 266, 11153-11157, 1991
A:Title: AP17 and AP19, the mammalian small chains of the clathrin-associated protein complex
A:Reference number: A40535; MUID:91250426
A:Accession: B40535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <KIR>
A:Cross-references: GB:M37194; NID:9202927; PIDN:AAA40742.1; PID:g202928
C:Superfamily: mouse clathrin-associated protein 19

Query Match 40.4%; Score 42; DB 2; Length 142;
Best Local Similarity 40.0%; Pred. No. 6;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAF 15
| | | | | | | | | |
DB 38 VVTVRDAKHTNFEV 52

RESULT 9
A28029
phosphoprotein phosphatase (EC 3.1.3.16) 2A catalytic chain - bovine
N:Alternate names: protein phosphatase-2A catalytic chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 04-Mar-2000
C:Accession: A28029
R.Green, D.D.; Yang, S.I.; Mumby, M.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 4880-4884, 1987
A:Title: Molecular cloning and sequence analysis of the catalytic subunit of bovine type 2 phosphoprotein phosphatase
A:Reference number: A28029; MUID:87260892
A:Accession: A28029
A:Molecule type: mRNA
A:Residues: 1-325 <GRE>
A:Cross-references: GB:M16968; NID:g163515; PIDN:AAA30695.1; PID:g163516
C:Superfamily: phosphoprotein phosphatase; phosphatase core homology; phosphoprotein
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphatase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His) #status predicted
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 40.4%; Score 42; DB 2; Length 325;
Best Local Similarity 53.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ITIRGSVHQNFA 14
| | | | | | | | | |
DB 52 VTVRGDVHGOFHD 64

RESULT 10
S69699
hypothetical protein YDR415c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001
C:Accession: S69699
R.Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and
A:Reference number: S69555
A:Accession: S69699
A:Molecule type: DNA
A:Residues: 1-374 <DIE>
A:Cross-references: EMBL:U33007; NID:g927713; GSPDB:GN00004; MIPS:YDR415
C:Genetics:
A:Gene: MIPS:YDR415C
A:Map position: 4R

Query Match 40.4%; Score 42; DB 2; Length 374;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 RGSVHQNFAFT 16
| | | | | | | | | |
DB 97 KGSMHKNLAKFT 108

RESULT 11
H84515
probable helicase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84515
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1230 <STO>
A:Cross-references: GB:AE002093; NID:g4406798; PIDN:AAD20107.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g14300
A:Map position: 2

Query Match 40.4%; Score 42; DB 2; Length 1230;
Best Local Similarity 38.9%; Pred. No. 76;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 TIRGSVHQNFAFTFATG 20
| | | | | | | | | |
DB 693 TVEGVVHKTYRDACYALG 710

RESULT 12
G71266
probable ATP-dependent nuclease, subunit A - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: G71266
R.Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.;
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.;

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770

A:Accession: G71266

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1239 <COL>

A:Cross-references: GB:AF001259; GB:AE000520; NID:g3323209; PIDN:AAC65853.1; PID:g3323209

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0898

Query Match

Best Local Similarity 40.4%; Score 42; DB 2; Length 1239;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 HQNEADTFEAT 19

Db 1132 HQFAEFSFLT 1142

RESULT 13

T15957

hypothetical protein F02E8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Mar-2001

C:Accession: T15957

R:Miller, N.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of C. elegans cosmid F02E8.

A:Reference number: Z18436

A:Accession: T15957

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-142 <MIL>

A:Cross-references: EMBL:U53340; NID:g1255859; PID:g1255861; PIDN:AAA96207.1; GSPDB:GN00

A:Experimental source: strain Bristol N2; clone F02E8

C:Genetics:

A:Gene: CESP:F02E8.3

A:Map position: X

A:Introns: 29/3; 89/3

C:Superfamily: mouse clathrin-associated protein 19

Query Match

Best Local Similarity 39.4%; Score 41; DB 2; Length 142;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ITIRGSVHQNFADF 15

Db 39 VTVRDAKHTNFEVF 52

RESULT 14

H86786

hypothetical protein yndB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001

C:Accession: H86786

R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich

Genome Res. in press, 2001

A:Title: The complete genome sequence of the lactic acid bacterium.

A:Reference number: A86625

A:Accession: H86786

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <STO>

A:Cross-references: GB:AE005176; NID:g12724273; PIDN:AAK05394.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yndB

Query Match 39.4%; Score 41; DB 2; Length 249;

Best Local Similarity 42.1%; Pred. NO. 19;

Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 ITIRGSVHQNFADTFATG 20

Db 204 ITIEGNGHSGFGSGFKG 222

RESULT 15

E71690

minor teichoic acids biosynthesis protein ggab (ggab) RP339 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Nov-2000

C:Accession: E71690

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsn

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria

A:Reference number: A71630; MUID:99039499

A:Accession: E71690

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-318 <AND>

A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14799.1; PID:g

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: ggab; RP339

C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match

Best Local Similarity 39.4%; Score 41; DB 1; Length 318;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MITIRGSVHQNFAD 14

Db 243 MIMIKGSTHQLSD 256

Search completed: March 9, 2002, 00:34:14

Job time: 325 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:47:38 ; Search time 30.16 Seconds
(without alignments)
24.314 Million cell updates/sec

Title: US-09-922-067-11

Perfect score: 104

Sequence: 1 MITIRGSVHQNFADFTFATG 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	441	1	PAFA_HUMAN
2	100	96.2	444	1	PAFA_CANFA
3	94	90.4	444	1	PAFA_BOVIN
4	86	82.7	436	1	PAFA_CAVPO
5	83	79.8	422	1	PAFA_CHICK
6	81	58.7	392	1	PAF2_HUMAN
7	59	56.7	392	1	PAF2_BOVIN
8	59	56.7	440	1	PAFA_MOUSE
9	54	51.9	476	1	PAFA_CAEEL
10	42	40.4	142	1	A2S1_HUMAN
11	42	40.4	142	1	A2S1_MOUSE
12	41	39.4	458	1	YM77_YEAST
13	40	38.5	296	1	THTR_MOUSE
14	40	38.5	579	1	ILVB_SPIPL
15	40	38.5	918	1	YNE6_CAEEL
16	39.5	38.0	540	1	TH16_YEAST
17	39.5	38.0	672	1	ANX6_RAT
18	39	37.5	178	1	Y449_HAEIN
19	39	37.5	438	1	SECV_METVA
20	39	37.5	466	1	HEMN_SYNY3
21	39	37.5	585	1	DCEH_YEAST
22	39	37.5	1216	1	YPX5_CAEEL
23	39	37.5	1239	1	V120_EBV
24	39	37.5	2201	1	TENA_HUMAN
25	39	37.5	3411	1	POLG_YEFV1
26	39	37.5	3411	1	POLG_YEFV2
27	38.5	37.0	475	1	GAPN_STRMO
28	38	36.5	184	1	YPS2_SYNP2
29	38	36.5	351	1	Y630_RICPR
30	38	36.5	382	1	YQF3_CAEEL
31	38	36.5	492	1	MURE_STAAU
32	38	36.5	731	1	DNLU_ZYMONA
33	37	35.6	121	1	YGIW_HAEIN

RESULT 1

ID	PAFA_HUMAN	STANDARD;	PRT;	441 AA.
AC	Q13093; Q15692;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)			
DE	(PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED			
DE	PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE			
DE	ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).			
GN	PLA2G7 OR PAFAH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.			
RC	TISSUE=Myeloid;			
RX	MEDLINE=95214779; PubMed=7700381;			
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,			
RA	Schjimpf B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,			
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;			
RT	"Anti-inflammatory properties of a platelet-activating factor			
RT	acetylhydrolase.";			
RL	Nature 374:549-553(1995).			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Lymphoma;			
RX	MEDLINE=96197208; PubMed=8624782;			
RA	Tew D.G., Southan C., Rice S.O.J., Lawrence M.P., Li H., Boyd H.F.,			
RA	Moore K., Gloger I.S., Macphie C.H.;			
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-			
RT	associated, serine-dependent phospholipase involved in the oxidative			
RT	modification of low-density lipoproteins.";			
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).			
RP	MUTAGENESIS.			
RX	MEDLINE=96029630; PubMed=7592717;			
RA	Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,			
RA	Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,			
RT	Gray P.W.;			
RT	"Plasma platelet-activating factor acetylhydrolase is a secreted			
RT	phospholipase A2 with a catalytic triad.";			
RL	J. Biol. Chem. 270:25481-25487(1995).			
RP	VARIANT PHE-279.			
RX	MEDLINE=96259525; PubMed=8675689;			
RA	Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W.,			
RA	Eberhardt C., Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A.,			
RA	McIntyre T.M., Gray P.W., Prescott S.M.;			
RT	"Platelet-activating factor acetylhydrolase deficiency. A missense			
RT	mutation near the active site of an anti-inflammatory			
RT	phospholipase.";			
RL	J. Clin. Invest. 97:2784-2791(1996).			
RP	[5]			

34	37	35.6	244	1	T2E5_ECOLI	P04390	escherichia
35	37	35.6	296	1	THTR_HUMAN	Q16762	homo sapien
36	37	35.6	303	1	PPV_DROME	Q27884	drosophila
37	37	35.6	305	1	PPP6_HUMAN	Q00743	homo sapien
38	37	35.6	305	1	PPP6_RAT	Q64620	rattus norv
39	37	35.6	325	1	ATP3_ARATH	Q96250	arabidopsis
40	37	35.6	385	1	FTS2_HELPJ	Q92km2	helicobacte
41	37	35.6	385	1	FTS2_HELPJ	P56097	helicobacte
42	37	35.6	397	1	POR_CHLRE	Q39617	chlamydomon
43	37	35.6	405	1	YRKO_BACSU	P54442	bacillus su
44	37	35.6	412	1	AK_PSEAE	O69077	pseudomonas
45	37	35.6	510	1	DDC_ACIBA	Q43908	acinetobact

ALIGNMENTS

RP VARIANT PHE-279.
RX MEDLINE-98430412; PubMed-9759612;
RA Yoshida H., Inaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
RA Yoshimizu N., Fukushi K., Satoh K.;
RT "A mutation in plasma platelet-activating factor acetylhydrolase
RT (Val279phe) is a genetic risk factor for cerebral hemorrhage but not
RL for hypertension.";
RL Thromb. Haemost. 80:372-375(1998).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- DISEASE: INHERITED DEFICIENCY OF PLA2G7 IS A TRAIT WHICH IS
CC PRESENT IN 27% OF JAPANESE. IT COULD HAVE A SIGNIFICANT
CC PHYSIOLOGIC EFFECT IN THE PRESENCE OF INFLAMMATORY BODILY
CC RESPONSES.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U20157; AAC50126.1; -;
CC DR EMBL; U24577; AAB04170.1; -;
CC DR MIM; 601690; -;
CC DR InterPro; IPR000379; Est_lip_thioest_actsite.
CC DR InterPro; IPR000734; Lipase.
CC DR PROSITE; PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
CC FT SIGNAL 1 21
CC FT CHAIN 22 441
CC FT ACT_SITE 273 273 PLATELET-ACTIVATING FACTOR
CC FT ACT_SITE 296 296 ACETYLDHROLASE.
CC FT ACT_SITE 351 351 CHARGE RELAY SYSTEM.
CC FT ACT_SITE 351 351 CHARGE RELAY SYSTEM.
CC FT CARBOHYD 423 423 CHARGE RELAY SYSTEM.
CC FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARIANT 279 279 V -> F (IN PLA2G7 DEFICIENCY; INACTIVE
CC PROTEIN).
CC FT FTID-VAR_004268.
CC FT MUTAGEN 108 108 S->A: ACTIVITY IS HIGHER THAN WILD TYPE.
CC FT MUTAGEN 273 273 S->A: LOSS OF ACTIVITY.
CC FT MUTAGEN 286 286 D->A: ALMOST NO ACTIVITY.
CC FT MUTAGEN 286 286 D->N: DIMINISHED ACTIVITY.
CC FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.
CC FT MUTAGEN 296 296 D->N: LOSS OF ACTIVITY.
CC FT MUTAGEN 304 304 D->A: NO CHANGE IN ACTIVITY.
CC FT MUTAGEN 338 338 D->A: ACTIVITY IS HIGHER THAN WILD TYPE.
CC FT MUTAGEN 351 351 H->A: LOSS OF ACTIVITY.
CC FT CONFLICT 379 379 V -> A (IN REF. 2).
CC SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;

Query Match 100.0%; Score 104; DB 1; Length 441;
Best Local Similarity 100.0%; Pred No. 2,7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MITIRGSVHQNFADFTFATG 20
|||||
Db 343 MITIRGSVHQNFADFTFATG 362

RESULT 2

PAFA_CANFA
ID PAFA_CANFA STANDARD; PRT; 444 AA.
AC Q28262;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-ACTIVATING FACTOR ACETYLDHROLASE PRECURSOR (EC 3.1.1.47)
DE (PAF ACETYLDHROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
DE ESTERASE) (1-ALKYL-2-ACETYLDHROLASE)
GN PLA2G7.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RX MEDLINE-96029630; PubMed-7592717;
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
CC PHOSPHOLIPIDS.
CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
CC H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U34246; AAC48484.1; -;
CC DR InterPro; IPR000379; Est_lip_thioest_actsite.
CC DR InterPro; IPR000734; Lipase.
CC DR PROSITE; PS00120; LIPASE_SER; 1.
CC KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
CC FT SIGNAL 1 21
CC FT CHAIN 22 444
CC FT ACT_SITE 274 274 PLATELET-ACTIVATING FACTOR
CC FT ACT_SITE 297 297 ACETYLDHROLASE.
CC FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT CARBOHYD 60 60 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 444 AA; 50136 MW; 814FE0AE38B074AC CRC64;

Query Match 96.2%; Score 100; DB 1; Length 444;
Best Local Similarity 95.0%; Pred. No. 1.3e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MITIRGSVHQNFADFTFATG 20
|||||
Db 344 MITIRGSVHQNFADFTTTC 363

RESULT 3
PAFA_BOVIN
ID PAFA_BOVIN STANDARD; PRT; 444 AA.

Q28017;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 20-AUG-2001 (Rel. 40, Last annotation update)
 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
 (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 PLA2G7.
 Bos taurus (Bovine).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Splice;
 MEDLINE=96029630; PubMed=7592717;
 Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 "Plasma platelet-activating factor acetylhydrolase is a secreted
 phospholipase A2 with a catalytic triad";
 J. Biol. Chem. 270:25481-25487(1995).
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).

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 or send an email to license@isb-sib.ch).

 EMBL: U34247; AAC48483.1; -
 InterPro: IPR000379; Est_lip_thioest_actsite.
 InterPro: IPR000734; Lipase.
 PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 444
 FT PLATELET-ACTIVATING FACTOR
 FT ACETYLHYDROLASE.
 FT ACT_SITE 274 274 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 297 297 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;
 SQ
 Query Match 90.4%; Score 94; DB 1; Length 444;
 Best Local Similarity 94.7%; Pred. No. 1.4e-08;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MITIRGSHQNFADFTFAT 19
 |||||
 Db 344 MITIRGSHQNFVDFTFAT 362
 RESULT 4
 PAFCA_CAVPO STANDARD; PRT; 436 AA.
 ID PAFCA_CAVPO

P70683;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 20-AUG-2001 (Rel. 40, Last annotation update)
 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
 (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 PLA2G7 OR PAFAH.
 Cavia porcellus (Guinea pig).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 NCBI_TaxID=10141;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=HARTLEY; TISSUE=Liver;
 MEDLINE=97103479; PubMed=8947850;
 Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
 Yokoyama K., Sekita M., Nojima S.;
 "Cloning, expression and characterization of plasma
 platelet-activating factor-acetylhydrolase from guinea pig";
 J. Biochem. 120:838-844(1996).
 CC -!- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 PHOSPHOLIPIDS.
 CC -!- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: PLASMA.
 CC -!- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).

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 EMBL: D67037; BA11054.1; -
 InterPro: IPR000379; Est_lip_thioest_actsite.
 InterPro: IPR000734; Lipase.
 PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 436
 FT PLATELET-ACTIVATING FACTOR
 FT ACETYLHYDROLASE.
 FT ACT_SITE 271 271 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 294 294 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 349 349 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 436 AA; 49062 MW; C359D96E392FEE11 CRC64;
 SQ
 Query Match 82.7%; Score 86; DB 1; Length 436;
 Best Local Similarity 75.0%; Pred. No. 3.2e-07;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MITIRGSHQNFADFTFATG 20
 |||||
 Db 341 MIAVKGSHVHNFDFTFATG 360
 RESULT 5
 PAFCA_CHICK STANDARD; PRT; 422 AA.
 ID PAFCA_CHICK
 AC Q90678;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U34278; AAC59717.1; -;
 DR InterPro; IPR000379; Est_lip_thioest_actsite.
 DR InterPro; IPR000734; Lipase.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 422
 FT PLATELET-ACTIVATING FACTOR
 FT ACETYLHYDROLASE.
 FT ACT_SITE 266 266
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 289 289
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 345 345
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 331 331
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376E9141 CRC64;

 Query Match 79.8%; Score 83; DB 1; Length 422;
 Best Local Similarity 75.0%; Pred. No. le-06;
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 QY 1 MITRIGSVHQNFADETFATG 20
 |||||:|||||:|||||:
 Db 337 MITRIGSVHQSFPDFTFVSG 356

 RESULT 6
 PAF2_HUMAN
 ID PAF2_HUMAN STANDARD; PRT; 392 AA.
 AC Q99487; 015458;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC

DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2) (HSD-PLA2).
 GN PAFAH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=971115847; PubMed=8955149;
 RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
 RA Aoki J., Hattori M., Arai H., Inoue K.;
 RT "CDNA cloning and expression of intracellular platelet-activating
 RT factor (PAF) acetylhydrolase II, its homology with plasma PAF
 RT acetylhydrolase.";
 RL J. Biol. Chem. 271:33032-33038(1996).
 RN [2]
 RP SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
 RC TISSUE=Prostate;
 RX MEDLINE=98161812; PubMed=9494101;
 RA Rice S.Q.J., Southern C., Boyd H.F., Terrett J.A., Macphree C.H.,
 RA Moores K., Gloger I.S., Tew D.G.;
 RT "Expression, purification and characterization of a human
 RT serine-dependent phospholipase A2 with high specificity for oxidized
 RT phospholipids and platelet activating factor.";
 RL Biochem. J. 330:1309-1315(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=97364701; PubMed=9218411;
 RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
 RA "Platelet-activating factor acetylhydrolases.";
 RL J. Biol. Chem. 272:17895-17898(1997).
 CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
 CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
 CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- ENZYME REGULATION: INHIBITED BY PHENYLMETHANESULFONYL FLUORIDE,
 CC 3,4-DICHLOROISOCOUMARIN, DIISOPROPYL FLUOROPHOSPHATE (DFP) AND
 CC DIETHYL P-NITROPHENYL PHOSPHATE (DENP).
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED IN DIFFERENT TISSUES, BUT
 CC HIGH IN B AND T LYMPHOCYTES. IN BRAIN, EXPRESSION IS RESTRICTED TO
 CC AMYGDALA AND FRONTAL CORTEX.
 CC -1- MASS SPECTROMETRY: MW=44162; METHOD=ELECTROSPRAY.
 CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D87845; BAA13468.1; -;
 DR EMBL; U89386; AAC39707.1; -;
 DR MIM; 602344; -;
 DR InterPro; IPR000379; Est_lip_thioest_actsite.
 DR InterPro; IPR000734; Lipase.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation.
 FT ACT_SITE 236 236
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 259 259
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 314 314
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CONFLICT 212 212
 FT L -> F (IN REF. 2).
 SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;

 Query Match 58.7%; Score 61; DB 1; Length 392;
 Best Local Similarity 55.0%; Pred. No. 0.0054;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MITIRGSHVHNFADFTFATG 20
 :||: ||||: || ||||

DB 306 IITVLGSHVHRSQDFAFVTC 325

RESULT 7
 ID PAF2_BOVIN STANDARD; PRT; 392 AA.
 AC P79106;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE 2, CYTOPLASMIC
 DE (EC 3.1.1.47) (SERINE DEPENDENT PHOSPHOLIPASE A2).
 GN PAF2
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=97115847; PubMed=8955149;
 RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
 RA Aoki J., Hattori M., Arai H., Inoue K.;
 RT "cDNA cloning and expression of intracellular platelet-activating
 RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
 RT acetylhydrolase.";
 RL J. Biol. Chem. 271:33032-33038(1996).
 RN [2]
 RP REVIEW.
 RX MEDLINE=97364701; PubMed=9218411;
 RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
 RA "Platelet-activating factor acetylhydrolases.";
 RL J. Biol. Chem. 272:17895-17898(1997).
 CC -1- FUNCTION: HAS A MARKED SELECTIVITY FOR PHOSPHOLIPIDS WITH SHORT
 CC ACYL CHAINS AT THE SN-2 POSITION. MAY SHARE A COMMON PHYSIOLOGIC
 CC FUNCTION WITH THE PLASMA-TYPE ENZYME.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVEL IN LIVER AND AT
 CC LOWER LEVELS IN OTHER TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE SERINE ESTERASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D87559; BAA13419.1; -;
 CC InterPro; IPR000379; Est_lip_thioest_actsite.
 CC PROSITE; PS00120; LIPASE_SER; 1.
 CC ACT_SITE 236 236 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 259 259 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 314 314 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC SEQUENCE 392 AA; 43865 MW; 1DEACA2ADFA4CEAB CRC64;

Query Match 56.7%; Score 59; DB 1; Length 392;
 Best Local Similarity 50.0%; Pred. No. 0.012;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MITIRGSHVHNFADFTFATG 20
 :||: ||||: || ||||

DB 306 IITVLGSHVHRSQDFAFVTC 325

RESULT 8
 ID PAF2_MOUSE STANDARD; PRT; 440 AA.
 AC Q60963;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (EC 3.1.1.47)
 DE (PAF ACETYLHYDROLASE) (PAF 2-ACYLHYDROLASE) (LDL-ASSOCIATED
 DE PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1-ALKYLGLYCEROPHOSPHOCHOLINE
 DE ESTERASE) (1-ALKYL-2-ACETYLGLYCEROPHOSPHOCHOLINE ESTERASE).
 GN PLA2G7 OR PAF2H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=96029630; PubMed=7592717;
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H.,
 RA Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M.,
 RA Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -1- FUNCTION: MODULATES THE ACTION OF PLATELET-ACTIVATING FACTOR (PAF)
 CC BY HYDROLYZING THE SN-2 ESTER BOND TO YIELD THE BIOLOGICALLY
 CC INACTIVE LYSO-PAF. HAS A SPECIFICITY FOR SUBSTRATES WITH A SHORT
 CC RESIDUE AT THE SN-2 POSITION. IT IS INACTIVE AGAINST LONG-CHAIN
 CC PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +
 CC H(2)O -> 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
 CC HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
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 CC
 CC EMBL; U34277; AAC52274.1; -;
 CC MGD; MGI:1351327; Pla2g7.
 CC InterPro; IPR000379; Est_lip_thioest_actsite.
 CC PROSITE; PS00120; LIPASE_SER; 1.
 CC ACT_SITE 22 22 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 295 295 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 350 350 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 59 59 N-LINKED (GLCNAC...) (POTENTIAL).
 CC ACT_SITE 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
 CC ACT_SITE 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

Query Match 56.7%; Score 59; DB 1; Length 440;
 Best Local Similarity 68.8%; Pred. No. 0.014;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 RGSVHNFADFTFATG 20
 :| |||| |||| ||

Db 346 QGLRHQNFDDFTFVTG 361

RESULT 9

PAFA_CAEEL	STANDARD:	PRT:	476 AA.
ID	Q22943;		
AC	Q22943;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE HOMOLOG (EC 3.1.1.47).		
GN	C52B9.7.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RN	STRAIN-BRISTOL N2;		
RC	Nelson J.;		
RA	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.		
RL	-1- CATALYTIC ACTIVITY: 2-ACETYL-1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE +		
CC	H(2)O = 1-ALKYL-SN-GLYCERO-3-PHOSPHOCHOLINE + ACETATE.		
CC	-1- SIMILARITY: STRONG, WITH VERTEBRATES PLATELET-ACTIVATING FACTOR		
CC	ACETYLHYDROLASE		
CC	-1- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,		
CC	HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).		
CC	-----		
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CC	cial entities requires a license agreement (See http://www.isb-sib.ch/announ		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; U64598; AAK39216.1; -		
DR	WormPep; C52B9.7; CE06966.		
DR	InterPro; IPR000379; Est_lip_thioest_actsite.		
DR	InterPro; IPR000734; Lipase.		
DR	PROSITE; PS00120; LIPASE_SER; FALSE_NEG.		
KW	Hypothetical protein; Hydrolyase; Lipid degradation.		
FT	ACT_SITE 326 326		
FT	ACT_SITE 349 349		
FT	ACT_SITE 404 404		
FT	SEQUENCE 476 AA; 53974 MW; D61DF01F396371F9 CRC64:		

Query Match	51.9%;	Score 54;	DB 1;	Length 476;
Best Local Similarity	56.2%;	Pred. NO. 0.11;		
Matches 9;	Conservative	4;	Mismatches	3; Indels

Qy 2 ITIRGSVHQNFADFTF 17
Db 397 LTLNGAVHQCFSDPEF 412

RESULT 10

AC	A2S1_HUMAN	STANDARD;	PRT;	142 AA.
ID	P53680;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	CLATHRIN COAT ASSEMBLY PROTEIN AP17 (CLATHRIN COAT ASSOCIATED PROTEIN AP17) (PLASMA MEMBRANE ADAPTOR AP-2 17 KDA PROTEIN) (HA2 17 KDA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN 2 SMALL CHAIN).			
GN	AP2S1 OR CLAPS2 OR AP17.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			

RP SEQUENCE FROM N. A.

SEQUENCE FROM N.A.
TISSUE=Kidney;
MEDLINE=97193186; PubMed=9040778;
Winterpacht A., Endeke S., Enklaar T., Fuhring M., Zabel B.;
"Human CLAPS2 encoding AP17, a small chain of the clathrin-associated
protein complex: cDNA cloning and chromosomal assignment to 19q13.2--
q13.3.";
Cytogenet. Cell Genet. 75:132-135(1996).
[2]
SEQUENCE FROM N.A.
MEDLINE=98440366; PubMed=9767099;
Holzmann K., Poeltl A., Sauerwald G.;
"A novel spliced transcript of human CLAPS2 encoding a protein
alternative to clathrin adaptor protein AP17.";
Gen. Funct. 2:39-44(1998).
-!- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
MEMBRANE PROTEINS LEADING TO THEIR SELECTION AND CONCENTRATION.
AP17 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
-!- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS A HETEROTETRAMER
COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN
(AP50) AND A SMALL CHAIN (AP17).
-!- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.
-!- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES SMALL SUBUNITS
FAMILY.

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or send an email to license@isb-sib.ch).

CC	EMBL; X97074; CAA65782.1; -
DR	EMBL; X97074; CAA65782.1; -
DR	EMBL; X97074; CAA65782.1; -
DR	EMBL; X97074; CAA65782.1; -
CC	EMBL; X97074; CAA65782.1; -

```
DR MIM; 602242; -.
DR InterPro; IPR000804; Clat_adaptor_s.
```

DR PF01217; Clat_adaptor_s; 1.
DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.

KW	Coated pits.
SQ	SEQUENCE 142 AA; 17018 MW: CA38A

Query Match	40.4%	Score 42;	DB 1;	Length 142;
Best Local Similarity	40.0%	Pred. No. 3.2;		

```
QY      1 MITIRGSVHQNFADF 15
          : : : : : : : : : :
Db     38 VVTVRDAKHTNFEVEF 52
```

11 JUL 54

A	ZS1_MOUSE		PRT;	142 AA.
R		STANDARD;		
E	ID A2S1_MOUSE			
S	AC Q00380;	P97626; P70626;		
I	DT 01-APR-1993	(Rel. 25, Created)		
L	DT 01-APR-1993	(Rel. 25, Last sequence update)		
N	DT 20-AUG-2001	(Rel. 40, Last annotation update)		
C	DE CLATHRIN COAT ASSEMBLY PROTEIN AP17			
O	DE AP17) (PLASMA MEMBRANE ADAPTOR AP-2 [CLATHRIN COAT ASSOCIATED PROTEIN			
D	DE SUBUNIT] (CLATHRIN ASSEMBLY PROTEIN 2 SMALL CHAIN).			
G	GN A2S1 OR CLAPS2 OR AP17.			
N	OS Mus musculus (Mouse), and			
C	QS Rattus norvegicus (Rat)..			
O	OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
X	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
C	NCBI_TaxID=10090, 10116;			
R	[1]			
R	RP SEQUENCE FROM N.A.			

RC SPECIES-Rat; TISSUE=Brain;
RX MEDLINE=91250426; PubMed=2040623;
RA Kirchhausen T., Davis A.C., Frucht S., O'Brine Greco B.,
RT Payne G.S., Tubb B.;
RA *AP17 and AP19, the mammalian small chains of the clathrin-associated
RT protein complexes show homology to Yap1/p, their putative homolog in
RL yeast.;
RT J. Biol. Chem. 266:111153-111157(1991).
RN [2]
RP SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
RA Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
RA Theising B., Wylie T., Lennon G., Soares B., Willson R., Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP17 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN
CC (AP50) AND A SMALL CHAIN (AP17).
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES SMALL SUBUNITS
CC FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC DE EMBL: M37194; AAA40742.1; -
CC DR EMBL: U75917; AAB46980.1; -
CC DR EMBL: AA277150; -; NOT_ANNOTATED_CDS.
CC DR PIR: B40535; B40535.
CC DR InterPro: IPR000804; clat_adaptor_s.
CC DR Pfam: PF01217; Clat_adaptor_s; 1.
CC DR PROSITE: PS00989; CLAT_ADAPTOR_S; 1.
CC KW Coated pits.
FT CONFLICT 83 83 A -> G (IN REF. 2).
FT CONFLICT 109 110 KV -> RF (IN REF. 2).
FT CONFLICT 117 117 M -> I (IN REF. 2).
FT CONFLICT 126 126 T -> R (IN REF. 2).
SQ SEQUENCE 142 AA; 17018 MW; CA3FD686C65AEDF6 CRC64;

Query Match 40.4%; Score 42; DB 1; Length 142;
Best Local Similarity 40.08; Pred. No. 3.2;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MITIRGSVHONFADF 15
Db 38 VVTVRDAKHNFVEF 52

RESULT 12

YMW7_YEAST
ID YMW7_YEAST STANDARD; PRT; 458 AA.
AC Q05031;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HYPOTHETICAL 50.5 KDA PROTEIN IN RNAI-RNT1 INTERGENIC REGION.
GN YMR238W OR YM9959.20.
OS Saccharomyces cerevisiae (Baker's yeast).
RA Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YKL046C.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC DR EMBL: Z49939; CAA90209.1; -
CC DR SGD: S0004851; YMR238W.
CC KW Hypothetical protein; Transmembrane.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 438 458 POTENTIAL.
SQ SEQUENCE 458 AA; 50540 MW; 908D7E672333EC03 CRC64;
Query Match 39.4%; Score 41; DB 1; Length 458;
Best Local Similarity 53.8%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 ITIRGSVHONFADF 14
Db 129 ITVMGAVERNFTD 141
RESULT 13
THTR_MOUSE
ID THTR_MOUSE STANDARD; PRT; 296 AA.
AC P52196;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE THIOSULFATE SULFURTRANSFERASE (EC 2.8.1.1) (RHODANESE).
GN TST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=96074596; PubMed=7488186;
RA Dooley T.P., Nair S.K., Garcia R.E., Courtney B.C.;
RT "Mouse rhodanese gene (Tst): cDNA cloning, sequencing, and
RT recombinant protein expression.";
RL Biochem. Biophys. Res. Commun. 216:1101-1109(1995).
CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
CC DETOXIFICATION.
CC -1- CATALYTIC ACTIVITY: THIOSULFATE + CYANIDE = SULFITE + THIOCYANATE.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -1- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
CC
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DR Pfam: PF01590; GAF; 1.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PD1ESTERASE1.
 DR SMART; SMO0085; GAF; 1.
 DR SMART; SMO0471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 KW Hypothetical protein; Hydrolase; cGMP.
 SQ SEQUENCE 918 AA; 104238 MW; CA59910AF4CD6155 CRC64;

Query Match 38.5%; Score 40; DB 1; Length 918;
 Best Local Similarity 87.5%; Pred. NO. 56;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 10 QNFADTF 17
 Db 423 QNFADFSF 430

Search completed: March 9, 2002, 00:47:39
 Job time: 800 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2002, 00:46:55 ; Search time 94.88 seconds
(without alignments)
30.833 Million cell updates/sec

Title: US-09-922-067-11

Perfect score: 104

Sequence: 1 MIIIRGSVHQNFADTFATG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_17:*
- 1: sp.archaea:*
 - 2: sp.bacteria:*
 - 3: sp.fungi:*
 - 4: sp.human:*
 - 5: sp.invertebrate:*
 - 6: sp.mammal:*
 - 7: sp.mhc:*
 - 8: sp.organelle:*
 - 9: sp.phage:*
 - 10: sp.plant:*
 - 11: sp.rodent:*
 - 12: sp.virus:*
 - 13: sp.vertebrate:*
 - 14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	55.8	384	5	O44753
2	52	50.0	541	10	Q9M3G4
3	52	50.0	830	10	Q9M184
4	52	50.0	996	10	Q9C925
5	45	43.3	303	4	Q9UC9
6	45	43.3	363	2	P94630
7	44	42.3	429	1	Q9HKS7
8	43	41.3	341	5	O45052
9	43	41.3	400	4	Q9C034
10	43	41.3	493	4	Q9C035
11	43	41.3	534	5	Q9GZF5
12	43	41.3	846	12	Q9YKS8
13	43	41.3	849	12	Q9YKR7
14	43	41.3	1669	10	Q9LW42
15	42.5	40.9	268	10	Q9FQ12
16	42.5	40.9	3396	5	Q9VM55
17	42	40.4	142	5	Q9VDC3
18	42	40.4	374	3	Q04033
19	42	40.4	515	10	O81639

20	42	40.4	1230	10	Q9ZQ61
21	42	40.4	1239	2	O83868
22	41	39.4	142	5	Q19123
23	41	39.4	249	2	Q9CG14
24	41	39.4	318	2	Q9ZDI9
25	41	39.4	367	2	P72900
26	40.5	38.9	554	12	Q98130
27	40	38.5	352	5	Q23345
28	40	38.5	379	11	O64627
29	40	38.5	425	2	P73829
30	40	38.5	463	2	O07346
31	40	38.5	463	2	P73374
32	40	38.5	599	2	Q9CF55
33	40	38.5	753	10	Q9C7M5
34	40	38.5	767	2	O25395
35	40	38.5	767	2	Q9ZLF4
36	40	38.5	942	6	Q9BDV5
37	39.5	38.0	213	2	O86734
38	39.5	38.0	342	11	Q9DA32
39	39.5	38.0	375	2	Q9F5P1
40	39.5	38.0	620	11	Q9DA68
41	39.5	38.0	777	5	O45373
42	39.5	38.0	920	3	Q02531
43	39.5	38.0	1172	5	O9VLG4
44	39	37.5	199	2	Q9HYW8
45	39	37.5	201	2	Q9L0M1

ALIGNMENTS

RESULT 1

O44753
ID O44753 PRELIMINARY: PRT; 384 AA.
AC O44753:
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE W03G9.6 PROTEIN.
GN W03G9.6.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smailson N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Dante M., Keppler D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF039716; AAB96738.1; -;
InterPro: IPR000379; Est_lip_thioest_actsite.

Q9ZQ61	arabidopsis
O83868	treponema p
Q19123	caenorhabdi
Q9CG14	lactococcus
Q9ZDI9	rickettsia
P72900	synecocyst
Q98V30	avian infec
Q23345	caenorhabdi
O64627	rattus norv
P73829	synecocyst
O07346	synecocyst
P73374	synecocyst
Q9CF55	lactococcus
Q9C7M5	arabidopsis
O25395	helicobacte
Q9ZLF4	helicobacte
Q9BDV5	manis sp. o
O86734	streptomyce
Q9DA32	mus musculu
O9F5P1	rhizobium m
Q9DA68	mus musculu
O45373	caenorhabdi
Q02531	schizophyll
O9VLG4	drosophila
Q9HYW8	pseudomonas
Q9L0M1	streptomyce

RP SEQUENCE FROM N.A.
A EU Arabidopsis sequencing project;
L Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RESULT	5
Q9UCI9	
D D	
C C	
Q9UCI9;	
01-MAY-2000	(TremblRel. 13, Created)
01-MAY-2000	(TremblRel. 13, Last sequence update)
01-JUN-2001	(TremblRel. 17, Last annotation update)
SERINE/THREONINE PROTEIN PHOSPHATASE CATALYTIC SUBUNIT	
PRELIMINARY;	PRT; 303 AA.

DR	InterPro: IPR001525; C5_DNA_meth.	
DR	Pfam: PF00145; DNA_methylase; 1.	
DR	PRINTS: PR00105; C5METTRFRASE.	
DR	PROSITE: PS00094; C5_MTASE_1; 1.	
DR	Methyltransferase; Restriction system; Transferase.	
FT	ACT_SITE 78 78 BY SIMILARITY.	
SQ	SEQUENCE 363 AA; 40746 MW; F6847A03D828D15A CRC64;	
Query Match	43.3%; Score 45; DB 2; Length 363;	
Best Local Similarity	57.1%; Pred. No. 9.5;	
Matches	8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
QY	5 RGSVHQNFADFTF 18	
Db	94 RGTLYQNFRDFVAA 107	
RESULT 7		
Q9HKS7		
ID	Q9HKS7 PRELIMINARY; PRT; 429 AA.	
AC	Q9HKS7;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	PROBABLE ASPARAGINYL--TRNA SYNTHETASE.	
GN	TX0519.	
OS	Thermoplasma acidophilum.	
OC	Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;	
OC	Thermoplasma.	
OX	NCBI_TaxID=2303;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=DSM 1728;	
RX	MEDLINE=20479972; PubMed=11029001;	
RA	Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,	
RA	Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumelster W.;	
RT	"The genome sequence of the thermoacidophilic scavenger Thermoplasma	
RT	acidophilum.";	
RL	Nature 407:508-513(2000).	
DR	EWEL; AL445064; CAC11659.1; "	
DR	InterPro: IPR002309; tRNA-synt_2.	
DR	InterPro: IPR002312; tRNA-synt_casp.	
Pfam; PF00152; tRNA-synt_2; 1.		
DR	Pfam; PF01336; tRNA_anti; 1.	
DR	PRINTS; PR01042; TRNASYNTHASP.	
KW	Aminoacyl-tRNA synthetase; Complete proteome.	
SQ	SEQUENCE 429 AA; 49947 MW; 266B477FCC0C32B6 CRC64;	
Query Match	42.3%; Score 44; DB 1; Length 429;	
Best Local Similarity	35.0%; Pred. No. 17;	
Matches	7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;	
QY	1 MITIRGSHQNFADFTFATG 20	
	::: ::: :	
Db	129 VLKIRSTIRSFADFFYENG 148	
RESULT 8		
O45052		
ID	O45052 PRELIMINARY; PRT; 341 AA.	
AC	O45052;	
DT	01-JUN-1998 (TREMBLrel. 06, Created)	
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	COSG6.3 PROTEIN.	
GN	COSG6.3.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderidae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RN	[1]	

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin K., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Kemp K.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045635; AAC02556.1; -;
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF00092; vwa; 1.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR PROSITE; PS50234; VWFA; 1.
 DR SMART; SM00327; VWA; 1.
 SQ SEQUENCE 341 AA; 37460 MW; 2FF07E14C5CCF5D4 CRC64;

Query Match 41.3%; Score 43; DB 5; Length 341;
 Best Local Similarity 57.1%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 IRGSVHONFADETF 17
 I I I I I I I I
 Db 312 ISGDVHHTFDVTF 325

RESULT 9
 Q9C034
 ID Q9C034 PRELIMINARY; PRT; 400 AA.
 AC Q9C034;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE TRIPARTITE MOTIF PROTEIN TRIM5 ISOFORM BETA.
 GN TRIM5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raymond A., Meroni G.;
 RT "Deciphering the function of the tripartite motif containing
 RT proteins";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF220026; AAG53480.1; -;
 SQ SEQUENCE 400 AA; 46037 MW; E8AC7B014BF58488 CRC64;

Query Match 41.3%; Score 43; DB 4; Length 400;
 Best Local Similarity 43.8%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 5 RGSVHONFADETFATG 20
 I I I I I I I I

Db 332 RGTRYQTFVNFNYCTG 347
 RESULT 10
 Q9C035
 ID Q9C035 PRELIMINARY; PRT; 493 AA.
 AC Q9C035;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE TRIPARTITE MOTIF PROTEIN TRIM5 ISOFORM ALPHA.
 GN TRIM5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raymond A., Meroni G.;
 RT "Deciphering the function of the tripartite motif containing
 RT proteins";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF220025; AAG53479.1; -;
 SQ SEQUENCE 493 AA; 56338 MW; 8561AAFD508AF6C0 CRC64;

Query Match 41.3%; Score 43; DB 4; Length 493;
 Best Local Similarity 43.8%; Pred. No. 31;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 RGSVHONFADETFATG 20
 I I I I I I I I
 Db 332 RGTRYQTFVNFNYCTG 347

RESULT 11
 Q9CZFS
 ID Q9CZFS PRELIMINARY; PRT; 534 AA.
 AC Q9CZFS;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE C18H7.1 PROTEIN.
 GN C18H7.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Tin-Wollam A., Fronick W.;
 RT "The sequence of C. elegans cosmid C18H7.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF067607; AAF98615.1; -;
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF00092; vwa; 2.
 DR SMART; SM00327; VWA; 2.
 DR PROSITE; PS50234; VWFA; 2.
 SQ SEQUENCE 534 AA; 59740 MW; E61DCA420962192E CRC64;

```

Query Match          41.3%; Score 43; DB 5; Length 534;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 IRGSVHQNFADTF 17
   | | | | | | | |
Db 505 ISGDVHHFTDVT 518

RESULT 12
Q9YKS8 PRELIMINARY; PRT; 846 AA.
ID Q9YKS8;
AC Q9YKS8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C-96Bw11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
RA Essex M.;
RA "Molecular Cloning and Phylogenetic Analysis of Human Immunodeficiency
RT Virus type 1 Subtype C: a Set of 23 Full-Length Clones from
RT Botswana.";
RL J. Virol. 0:0-0(1999).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C-96Bw11.04;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
RA Foley B.T., Ndung'u T.P., Marlink R., Essex M.;
RA Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110969; AAD17093.1; -
DR InterPro; IPR000328; Env-GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF005516; GP120; 1.
DR Pfam; PF005517; GP41; 1.
DR SQ SEQUENCE 846 AA; 96283 MW; AD196033D328ED3C CRC64;

Query Match          41.3%; Score 43; DB 12; Length 846;
Best Local Similarity 46.2%; pred. No. 58;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ITIRGSVHQNFAD 14
   | | : | | | |
Db 133 VTVDNLHQNFDT 145

RESULT 13
Q9YKR7 PRELIMINARY; PRT; 849 AA.
ID Q9YKR7
AC Q9YKR7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=C-96Bw11B01;
RA Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

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DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DE 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE LECTIN-RELATED PROTEIN PRECURSOR.
 OS Citrus paradisi (Grapefruit).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 OX NCBT_TaxID-37656;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MARSH; TISSUE=2-5 GRAM FRUIT YOUNG FLAVEDO;
 RA Sinisterra X.H., Shatters R.G. Jr., McCollum T.G., Doostdar H.,
 RA Mayer R.T.;
 RT "Expression of lectin homolog in grapefruit flavedo."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF283537; AAG38522.1;
 DR InterPro; IPR000985; Lectin_legA.
 DR InterPro; IPR01220; Lectin_legB.
 DR Pfam; PF00138; lectin_legA; 1
 DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 SQ SEQUENCE 268 AA; 29147 MW; 0353BCA4B96A9F27 CRC64;

Query Match 40.9%; Score 42.5; DB 10; Length 268;
 Best Local Similarity 44.0%; Pred. No. 19;
 Matches 11; Conservative 3; Mismatches 4; Indels 7; Gaps 1;
 QY 2 ITIRGSVHONFAD-----FTFAT 19
 III:|III:|
 Db 89 ITIKIRHONYTRAGDGMTIFAS 113

Search completed: March 9, 2002, 00:46:58
 Job time: 834 sec